

!!AA MULTIPLE ALIGNMENT 1.0  
 Pileup of: us\*

Symbol comparison table: GenRunData:blosum62.cmp CompCheck: 1102

GapWeight: 8  
 GapLengthWeight: 0

pileup.msf MSF: 1222 Type: P December 17, 2003 13:31 Check: 3612 ..

Name: us-09-873-409-3 Len: 1222 Check: 8709 Weight: 1.00  
 Name: us-09-873-409-7 Len: 1222 Check: 4278 Weight: 1.00  
 Name: us-09-873-409-8 Len: 1222 Check: 9292 Weight: 1.00  
 Name: us-09-873-409-1 Len: 1222 Check: 5986 Weight: 1.00  
 Name: us-09-873-409-2 Len: 1222 Check: 1428 Weight: 1.00  
 Name: us-09-873-409-4 Len: 1222 Check: 4911 Weight: 1.00  
 Name: us-09-873-409-5 Len: 1222 Check: 6997 Weight: 1.00  
 Name: us-09-873-409-6 Len: 1222 Check: 2011 Weight: 1.00

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1 50

us-09-873-409-3 MGLIASLV NGACLPMLP VLGEMSDNLI SGCLVQNTY SEFRLLYYV  
 us-09-873-409-7 MGLIASLV NGACLPMLP VLGEMSDNLI SGCLVQNTY SEFRLLYYV  
 us-09-873-409-8 MGLIASLV NGACLPMLP VLGEMSDNLI SGCLVQNTY SEFRLLYYV  
 us-09-873-409-1 MGLIASLV NGACLPMLP VLGEMSDNLI SGCLVQNTY SEFRLLYYV  
 us-09-873-409-2 MGLIASLV NGACLPMLP VLGEMSDNLI SGCLVQNTY SEFRLLYYV  
 us-09-873-409-4 MGLIASLV NGACLPMLP VLGEMSDNLI SGCLVQNTY SEFRLLYYV  
 us-09-873-409-5 MGLIASLV NGACLPMLP VLGEMSDNLI SGCLVQNTY SEFRLLYYV  
 us-09-873-409-6 MGLIASLV NGACLPMLP VLGEMSDNLI SGCLVQNTY SEFRLLYYV

51 100

us-09-873-409-3 GIGVALING YIQISLMIIT AAROTKIRK QPFSVLAOD IGMPSCDIG  
 us-09-873-409-7 GIGVALING YIQISLMIIT AAROTKIRK QPFSVLAOD IGMPSCDIG  
 us-09-873-409-8 GIGVALING YIQISLMIIT AAROTKIRK QPFSVLAOD IGMPSCDIG  
 us-09-873-409-1 GIGVALING YIQISLMIIT AAROTKIRK QPFSVLAOD IGMPSCDIG  
 us-09-873-409-2 GIGVALING YIQISLMIIT AAROTKIRK QPFSVLAOD IGMPSCDIG  
 us-09-873-409-4 GIGVALING YIQISLMIIT AAROTKIRK QPFSVLAOD IGMPSCDIG  
 us-09-873-409-5 GIGVALING YIQISLMIIT AAROTKIRK QPFSVLAOD IGMPSCDIG  
 us-09-873-409-6 GIGVALING YIQISLMIIT AAROTKIRK QPFSVLAOD IGMPSCDIG

101 150

us-09-873-409-3 ELNTRMTDID KISDGIQDKI ALFRONMSTF SIGLAVALK GKKLTLYTIS  
 us-09-873-409-7 ELNTRMTDID KISDGIQDKI ALFRONMSTF SIGLAVALK GKKLTLYTIS  
 us-09-873-409-8 ELNTRMTDID KISDGIQDKI ALFRONMSTF SIGLAVALK GKKLTLYTIS  
 us-09-873-409-1 ELNTRMTDID KISDGIQDKI ALFRONMSTF SIGLAVALK GKKLTLYTIS  
 us-09-873-409-2 ELNTRMTDID KISDGIQDKI ALFRONMSTF SIGLAVALK GKKLTLYTIS  
 us-09-873-409-4 ELNTRMTDID KISDGIQDKI ALFRONMSTF SIGLAVALK GKKLTLYTIS  
 us-09-873-409-5 ELNTRMTDID KISDGIQDKI ALFRONMSTF SIGLAVALK GKKLTLYTIS  
 us-09-873-409-6 ELNTRMTDID KISDGIQDKI ALFRONMSTF SIGLAVALK GKKLTLYTIS

151 200

us-09-873-409-3 TSPILMASAA ACSRWISLT SKELSAVSKA GAAVEVLSS IRTVIAFRAQ  
 us-09-873-409-7 TSPILMASAA ACSRWISLT SKELSAVSKA GAAVEVLSS IRTVIAFRAQ  
 us-09-873-409-8 TSPILMASAA ACSRWISLT SKELSAVSKA GAAVEVLSS IRTVIAFRAQ  
 us-09-873-409-1 TSPILMASAA ACSRWISLT SKELSAVSKA GAAVEVLSS IRTVIAFRAQ  
 us-09-873-409-2 TSPILMASAA ACSRWISLT SKELSAVSKA GAAVEVLSS IRTVIAFRAQ  
 us-09-873-409-4 TSPILMASAA ACSRWISLT SKELSAVSKA GAAVEVLSS IRTVIAFRAQ  
 us-09-873-409-5 TSPILMASAA ACSRWISLT SKELSAVSKA GAAVEVLSS IRTVIAFRAQ  
 us-09-873-409-6 TSPILMASAA ACSRWISLT SKELSAVSKA GAAVEVLSS IRTVIAFRAQ

201 250

us-09-873-409-3 EKELQSPFL NITRYAMPF PÖMLISCYLX FVRYTÖULKD AADPGIKRTI  
 us-09-873-409-7 EKELQSPFL NITRYAMPF PÖMLISCYLX FVRYTÖULKD AADPGIKRTI  
 us-09-873-409-8 EKELQSPFL NITRYAMPF PÖMLISCYLX FVRYTÖULKD AADPGIKRTI  
 us-09-873-409-1 EKELQSPFL NITRYAMPF PÖMLISCYLX FVRYTÖULKD AADPGIKRTI  
 us-09-873-409-2 EKELQSPFL NITRYAMPF PÖMLISCYLX FVRYTÖULKD AADPGIKRTI  
 us-09-873-409-4 EKELQSPFL NITRYAMPF PÖMLISCYLX FVRYTÖULKD AADPGIKRTI  
 us-09-873-409-5 EKELQSPFL NITRYAMPF PÖMLISCYLX FVRYTÖULKD AADPGIKRTI  
 us-09-873-409-6 EKELQSPFL NITRYAMPF PÖMLISCYLX FVRYTÖULKD AADPGIKRTI

us-09-873-409-3 251 300

us-09-873-409-7 ASKVSIGAVY FPMNGTYGIA FMYGTSILIN GERGYITGV LAVPSVHIS  
 us-09-873-409-8 ASKVSIGAVY FPMNGTYGIA FMYGTSILIN GERGYITGV LAVPSVHIS  
 us-09-873-409-1 ASKVSIGAVY FPMNGTYGIA FMYGTSILIN GERGYITGV LAVPSVHIS  
 us-09-873-409-2 ASKVSIGAVY FPMNGTYGIA FMYGTSILIN GERGYITGV LAVPSVHIS  
 us-09-873-409-4 ASKVSIGAVY FPMNGTYGIA FMYGTSILIN GERGYITGV LAVPSVHIS  
 us-09-873-409-5 ASKVSIGAVY FPMNGTYGIA FMYGTSILIN GERGYITGV LAVPSVHIS  
 us-09-873-409-6 ASKVSIGAVY FPMNGTYGIA FMYGTSILIN GERGYITGV LAVPSVHIS

301 350

us-09-873-409-3 SYCIGAAPH PETPAIARGA AFHIFÖYIDK KPSIDNPSTK GKPSISIBST  
 us-09-873-409-7 SYCIGAAPH PETPAIARGA AFHIFÖYIDK KPSIDNPSTK GKPSISIBST  
 us-09-873-409-8 SYCIGAAPH PETPAIARGA AFHIFÖYIDK KPSIDNPSTK GKPSISIBST  
 us-09-873-409-1 SYCIGAAPH PETPAIARGA AFHIFÖYIDK KPSIDNPSTK GKPSISIBST  
 us-09-873-409-2 SYCIGAAPH PETPAIARGA AFHIFÖYIDK KPSIDNPSTK GKPSISIBST  
 us-09-873-409-4 SYCIGAAPH PETPAIARGA AFHIFÖYIDK KPSIDNPSTK GKPSISIBST  
 us-09-873-409-5 SYCIGAAPH PETPAIARGA AFHIFÖYIDK KPSIDNPSTK GKPSISIBST  
 us-09-873-409-6 SYCIGAAPH PETPAIARGA AFHIFÖYIDK KPSIDNPSTK GKPSISIBST

351 400

us-09-873-409-3 VERKVSFMY PSRPSIKILK GLNLRISGE TVALVGLNGS GKSTVÖLLQ  
 us-09-873-409-7 VERKVSFMY PSRPSIKILK GLNLRISGE TVALVGLNGS GKSTVÖLLQ  
 us-09-873-409-8 VERKVSFMY PSRPSIKILK GLNLRISGE TVALVGLNGS GKSTVÖLLQ  
 us-09-873-409-1 VERKVSFMY PSRPSIKILK GLNLRISGE TVALVGLNGS GKSTVÖLLQ  
 us-09-873-409-2 VERKVSFMY PSRPSIKILK GLNLRISGE TVALVGLNGS GKSTVÖLLQ  
 us-09-873-409-4 VERKVSFMY PSRPSIKILK GLNLRISGE TVALVGLNGS GKSTVÖLLQ  
 us-09-873-409-5 VERKVSFMY PSRPSIKILK GLNLRISGE TVALVGLNGS GKSTVÖLLQ  
 us-09-873-409-6 VERKVSFMY PSRPSIKILK GLNLRISGE TVALVGLNGS GKSTVÖLLQ

401 450

us-09-873-409-3 WYENDIRAL NVRYRHIG VWSQBPVLFG TTISNNIKYG  
 us-09-873-409-7 WYENDIRAL NVRYRHIG VWSQBPVLFG TTISNNIKYG  
 us-09-873-409-8 WYENDIRAL NVRYRHIG VWSQBPVLFG TTISNNIKYG  
 us-09-873-409-1 WYENDIRAL NVRYRHIG VWSQBPVLFG TTISNNIKYG  
 us-09-873-409-2 WYENDIRAL NVRYRHIG VWSQBPVLFG TTISNNIKYG  
 us-09-873-409-4 WYENDIRAL NVRYRHIG VWSQBPVLFG TTISNNIKYG  
 us-09-873-409-5 WYENDIRAL NVRYRHIG VWSQBPVLFG TTISNNIKYG  
 us-09-873-409-6 WYENDIRAL NVRYRHIG VWSQBPVLFG TTISNNIKYG

451 500

us-09-873-409-3 RODVYDEEME RAAREANAYD FIMEFPKFN TLVGEKAOM SGOQORINAI  
 us-09-873-409-7 RODVYDEEME RAAREANAYD FIMEFPKFN TLVGEKAOM SGOQORINAI  
 us-09-873-409-8 RODVYDEEME RAAREANAYD FIMEFPKFN TLVGEKAOM SGOQORINAI  
 us-09-873-409-1 RODVYDEEME RAAREANAYD FIMEFPKFN TLVGEKAOM SGOQORINAI  
 us-09-873-409-2 RODVYDEEME RAAREANAYD FIMEFPKFN TLVGEKAOM SGOQORINAI  
 us-09-873-409-4 RODVYDEEME RAAREANAYD FIMEFPKFN TLVGEKAOM SGOQORINAI  
 us-09-873-409-5 RODVYDEEME RAAREANAYD FIMEFPKFN TLVGEKAOM SGOQORINAI  
 us-09-873-409-6 RODVYDEEME RAAREANAYD FIMEFPKFN TLVGEKAOM SGOQORINAI

501 550

us-09-873-409-3 ARLAVNPCKI LILDEATSAL DSEBSKAVOA ALEKDT  
 us-09-873-409-7 ARLAVNPCKI LILDEATSAL DSEBSKAVOA ALEKDT  
 us-09-873-409-8 ARLAVNPCKI LILDEATSAL DSEBSKAVOA ALEKDT  
 us-09-873-409-1 ARLAVNPCKI LILDEATSAL DSEBSKAVOA ALEKDT  
 us-09-873-409-2 ARLAVNPCKI LILDEATSAL DSEBSKAVOA ALEKDT  
 us-09-873-409-4 ARLAVNPCKI LILDEATSAL DSEBSKAVOA ALEKDT  
 us-09-873-409-5 ARLAVNPCKI LILDEATSAL DSEBSKAVOA ALEKDT  
 us-09-873-409-6 ARLAVNPCKI LILDEATSAL DSEBSKAVOA ALEKDT

551 600

us-09-873-409-3 HIAERGA HABLMAERGL YSLVWSODI KKADEQMESM  
 us-09-873-409-7 HIAERGA HABLMAERGL YSLVWSODI KKADEQMESM  
 us-09-873-409-8 HIAERGA HABLMAERGL YSLVWSODI KKADEQMESM  
 us-09-873-409-1 HIAERGA HABLMAERGL YSLVWSODI KKADEQMESM  
 us-09-873-409-2 HIAERGA HABLMAERGL YSLVWSODI KKADEQMESM  
 us-09-873-409-4 HIAERGA HABLMAERGL YSLVWSODI KKADEQMESM  
 us-09-873-409-5 HIAERGA HABLMAERGL YSLVWSODI KKADEQMESM  
 us-09-873-409-6 HIAERGA HABLMAERGL YSLVWSODI KKADEQMESM

601 650

us-09-873-409-3 TYSTERKTNS LPLHSVKSIX SDFIDKAES TÖSKETISLPE VSLKILKILN  
 us-09-873-409-7 TYSTERKTNS LPLHSVKSIX SDFIDKAES TÖSKETISLPE VSLKILKILN  
 us-09-873-409-8 TYSTERKTNS LPLHSVKSIX SDFIDKAES TÖSKETISLPE VSLKILKILN  
 us-09-873-409-1 TYSTERKTNS LPLHSVKSIX SDFIDKAES TÖSKETISLPE VSLKILKILN

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us-09-873-409-2 TYSTERKTN LPLHVSXIK SDFIDKABS TOSKEISLPE VSLIKLIKLN
us-09-873-409-4 TYSTERKTN LPLHVSXIK SDFIDKABS TOSKEISLPE VSLIKLIKLN
us-09-873-409-5 TYSTERKTN LPLHVSXIK SDFIDKABS TOSKEISLPE VSLIKLIKLN
us-09-873-409-6 TYSTERKTN LPLHVSXIK SDFIDKABS TOSKEISLPE VSLIKLIKLN

651
us-09-873-409-3 ..... 700
us-09-873-409-7 .....
us-09-873-409-8 KPEMPFVLG TLASVANGTV HVPFSLIPAK IITFNGNDK TTKHDAEIV
us-09-873-409-1 KPEMPFVLG TLASVANGTV HVPFSLIPAK IITFNGNDK TTKHDAEIV
us-09-873-409-2 KPEMPFVLG TLASVANGTV HVPFSLIPAK IITFNGNDK TTKHDAEIV
us-09-873-409-4 KPEMPFVLG TLASVANGTV HVPFSLIPAK IITFNGNDK TTKHDAEIV
us-09-873-409-5 KPEMPFVLG TLASVANGTV HVPFSLIPAK IITFNGNDK TTKHDAEIV
us-09-873-409-6 KPEMPFVLG TLASVANGTV HVPFSLIPAK IITFNGNDK TTKHDAEIV

701
us-09-873-409-3 ..... 750
us-09-873-409-7 .....
us-09-873-409-8 SMIFVILGVI CPVSFPMOGL FYGRAGEILT MLRHLAPKA MLYODIAMPD
us-09-873-409-1 SMIFVILGVI CPVSFPMOGL FYGRAGEILT MLRHLAPKA MLYODIAMPD
us-09-873-409-2 SMIFVILGVI CPVSFPMOGL FYGRAGEILT MLRHLAPKA MLYODIAMPD
us-09-873-409-4 SMIFVILGVI CPVSFPMOGL FYGRAGEILT MLRHLAPKA MLYODIAMPD
us-09-873-409-5 SMIFVILGVI CPVSFPMOGL FYGRAGEILT MLRHLAPKA MLYODIAMPD
us-09-873-409-6 SMIFVILGVI CPVSFPMOGL FYGRAGEILT MLRHLAPKA MLYODIAMPD

751
us-09-873-409-3 ..... 800
us-09-873-409-7 .....
us-09-873-409-8 EKENSTGGLT TILAIDIAOI OGATSRIGV LTONATNNGL SVIISFYGM
us-09-873-409-1 EKENSTGGLT TILAIDIAOI OGATSRIGV LTONATNNGL SVIISFYGM
us-09-873-409-2 EKENSTGGLT TILAIDIAOI OGATSRIGV LTONATNNGL SVIISFYGM
us-09-873-409-4 EKENSTGGLT TILAIDIAOI OGATSRIGV LTONATNNGL SVIISFYGM
us-09-873-409-5 EKENSTGGLT TILAIDIAOI OGATSRIGV LTONATNNGL SVIISFYGM
us-09-873-409-6 EKENSTGGLT TILAIDIAOI OGATSRIGV LTONATNNGL SVIISFYGM

801
us-09-873-409-3 ..... 850
us-09-873-409-7 .....
us-09-873-409-8 EMTFLILISIA PVLAVTGMIE TAAMTGFAK DKOELKHAGK IATEALENIR
us-09-873-409-1 EMTFLILISIA PVLAVTGMIE TAAMTGFAK DKOELKHAGK IATEALENIR
us-09-873-409-2 EMTFLILISIA PVLAVTGMIE TAAMTGFAK DKOELKHAGK IATEALENIR
us-09-873-409-4 EMTFLILISIA PVLAVTGMIE TAAMTGFAK DKOELKHAGK IATEALENIR
us-09-873-409-5 EMTFLILISIA PVLAVTGMIE TAAMTGFAK DKOELKHAGK IATEALENIR
us-09-873-409-6 EMTFLILISIA PVLAVTGMIE TAAMTGFAK DKOELKHAGK IATEALENIR

851
us-09-873-409-3 ..... 900
us-09-873-409-7 .....
us-09-873-409-8 TIVSLTREKA FEOMYEBMLO TOHRNTSKA QIISCVAFS HAFIYFAYAA
us-09-873-409-1 TIVSLTREKA FEOMYEBMLO TOHRNTSKA QIISCVAFS HAFIYFAYAA
us-09-873-409-2 TIVSLTREKA FEOMYEBMLO TOHRNTSKA QIISCVAFS HAFIYFAYAA
us-09-873-409-4 TIVSLTREKA FEOMYEBMLO TOHRNTSKA QIISCVAFS HAFIYFAYAA
us-09-873-409-5 TIVSLTREKA FEOMYEBMLO TOHRNTSKA QIISCVAFS HAFIYFAYAA
us-09-873-409-6 TIVSLTREKA FEOMYEBMLO TOHRNTSKA QIISCVAFS HAFIYFAYAA

901
us-09-873-409-3 ..... 950
us-09-873-409-7 ..... PRYS.....
us-09-873-409-8 GFRGAVILIO AGMTPEBGMF IVFTALAYGA MAIGKIVILA PEYSKAKSGA
us-09-873-409-1 GFRGAVILIO AGMTPEBGMF IVFTALAYGA MAIGKIVILA PEYSKAKSGA
us-09-873-409-2 GFRGAVILIO AGMTPEBGMF IVFTALAYGA MAIGKIVILA PEYSKAKSGA
us-09-873-409-4 GFRGAVILIO AGMTPEBGMF IVFTALAYGA MAIGKIVILA PEYSKAKSGA
us-09-873-409-5 GFRGAVILIO AGMTPEBGMF IVFTALAYGA MAIGKIVILA PEYSKAKSGA
us-09-873-409-6 GFRGAVILIO AGMTPEBGMF IVFTALAYGA MAIGKIVILA PEYSKAKSGA

951
us-09-873-409-3 ..... 1000
us-09-873-409-7 .....
us-09-873-409-8 AHLFALLEKK PNIDSRQOG KKPDTCEGNL EPREVSFPYP CRPDVFTLRG
us-09-873-409-1 AHLFALLEKK PNIDSRQOG KKPDTCEGNL EPREVSFPYP CRPDVFTLRG
us-09-873-409-2 AHLFALLEKK PNIDSRQOG KKPDTCEGNL EPREVSFPYP CRPDVFTLRG
us-09-873-409-4 AHLFALLEKK PNIDSRQOG KKPDTCEGNL EPREVSFPYP CRPDVFTLRG
us-09-873-409-5 AHLFALLEKK PNIDSRQOG KKPDTCEGNL EPREVSFPYP CRPDVFTLRG
us-09-873-409-6 AHLFALLEKK PNIDSRQOG KKPDTCEGNL EPREVSFPYP CRPDVFTLRG

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us-09-873-409-6 AHLFALLEKK PNIDSRQOG KKPDTCEGNL EPREVSFPYP CRPDVFTLRG

1001
us-09-873-409-3 ..... 1050
us-09-873-409-7 .....
us-09-873-409-8 LSLISIRGKT VAFVSSSGG KSTSVOLLOR LYDPVOGOVL FGVDKAEIN
us-09-873-409-1 LSLISIRGKT VAFVSSSGG KSTSVOLLOR LYDPVOGOVL FGVDKAEIN
us-09-873-409-2 LSLISIRGKT VAFVSSSGG KSTSVOLLOR LYDPVOGOVL FGVDKAEIN
us-09-873-409-4 LSLISIRGKT VAFVSSSGG KSTSVOLLOR LYDPVOGOVL FGVDKAEIN
us-09-873-409-5 LSLISIRGKT VAFVSSSGG KSTSVOLLOR LYDPVOGOVL FGVDKAEIN
us-09-873-409-6 LSLISIRGKT VAFVSSSGG KSTSVOLLOR LYDPVOGOVL FGVDKAEIN

1051
us-09-873-409-3 ..... 1100
us-09-873-409-7 .....
us-09-873-409-8 VOMLRQOIAI VPQEPVLENC SIAENIAYGD NSRVVPLDEI KEAANANIH
us-09-873-409-1 VOMLRQOIAI VPQEPVLENC SIAENIAYGD NSRVVPLDEI KEAANANIH
us-09-873-409-2 VOMLRQOIAI VPQEPVLENC SIAENIAYGD NSRVVPLDEI KEAANANIH
us-09-873-409-4 VOMLRQOIAI VPQEPVLENC SIAENIAYGD NSRVVPLDEI KEAANANIH
us-09-873-409-5 VOMLRQOIAI VPQEPVLENC SIAENIAYGD NSRVVPLDEI KEAANANIH
us-09-873-409-6 VOMLRQOIAI VPQEPVLENC SIAENIAYGD NSRVVPLDEI KEAANANIH

1101
us-09-873-409-3 ..... 1150
us-09-873-409-7 .....
us-09-873-409-8 SFIEGLPEKY NTQOVGLKGAO LSGQOKORIA IARALLQPK IILLDEATSA
us-09-873-409-1 SFIEGLPEKY NTQOVGLKGAO LSGQOKORIA IARALLQPK IILLDEATSA
us-09-873-409-2 SFIEGLPEKY NTQOVGLKGAO LSGQOKORIA IARALLQPK IILLDEATSA
us-09-873-409-4 SFIEGLPEKY NTQOVGLKGAO LSGQOKORIA IARALLQPK IILLDEATSA
us-09-873-409-5 SFIEGLPEKY NTQOVGLKGAO LSGQOKORIA IARALLQPK IILLDEATSA
us-09-873-409-6 SFIEGLPEKY NTQOVGLKGAO LSGQOKORIA IARALLQPK IILLDEATSA

1151
us-09-873-409-3 ..... 1200
us-09-873-409-7 .....
us-09-873-409-8 LNDSEKVOV HALDKARTGR TGLVWTRHLS AIONADILIV LHNGKIKEOG
us-09-873-409-1 LNDSEKVOV HALDKARTGR TGLVWTRHLS AIONADILIV LHNGKIKEOG
us-09-873-409-2 LNDSEKVOV HALDKARTGR TGLVWTRHLS AIONADILIV LHNGKIKEOG
us-09-873-409-4 LNDSEKVOV HALDKARTGR TGLVWTRHLS AIONADILIV LHNGKIKEOG
us-09-873-409-5 LNDSEKVOV HALDKARTGR TGLVWTRHLS AIONADILIV LHNGKIKEOG
us-09-873-409-6 LNDSEKVOV HALDKARTGR TGLVWTRHLS AIONADILIV LHNGKIKEOG

1201
us-09-873-409-3 ..... 1222
us-09-873-409-7 ..... F-----
us-09-873-409-8 THOELLANRD IYFKLVNAQS VO
us-09-873-409-1 THOELLANRD IYFKLVNAQS VO
us-09-873-409-2 THOELLANRD IYFKLVNAQS VO
us-09-873-409-4 THOELLANRD IYFKLVNAQS VO
us-09-873-409-5 THOELLANRD IYFKLVNAQS VO
us-09-873-409-6 THOELLANRD IYFKLVNAQS VO

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11AA MULTIPLE ALIGNMENT 1.0  
Pileup of: us\*

Symbol comparison table: GenRunData:blosum62.cmp CompCheck: 1102

GapWeight: 8  
GapLengthWeight: 0

p1leup2.msf MSF: 1222 Type: P December 17, 2003 13:38 Check: 8425 ..  
Name: us-09-873-409-2 Len: 1222 Check: 1428 Weight: 1.00  
Name: us-09-873-409-5 Len: 1222 Check: 6997 Weight: 1.00

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us-09-873-409-2 1 ----- 50
us-09-873-409-5 MIIIGILASLV NGACLPIMPL VLGEMSDNLI SGCLVQNTY SPFRLLTYV
51 ----- 100
us-09-873-409-2 GIGVALIFG YIQISLMTT AARQTKIRK QFFHSVLAQD IGMFSDCDIG
101 ----- 150
us-09-873-409-5 ELNTRMTDID KISDGIGDKI ALLFQNMSTF SIGLAVGLVK GMLKTLVTIS
151 ----- 200
us-09-873-409-2 TSPLIMASAA ACSRWISLT SKELSAVSKA GAVAEVLSS IRTVIAFRQ
201 ----- 250
us-09-873-409-5 EKELQSRFLL NITRYAMPYF POWLSCVLA FRYTQNLKD ADQFGIKRTI
251 ----- 300
us-09-873-409-2 ASKVSIGAVY FFMNGTYGIA FMYGTSLLN GERPTTIGV LAFPSVTHS
301 ----- 350
us-09-873-409-5 SYCIGAVPH FETPAIARGA AFHIFQVIDK KPSIDNSTA GYKPESEIGT
351 ----- 400
us-09-873-409-2 VERKNVSFNT PSRPSIKILK GINLRIKSGE TVALVGLNGS GKSTVQLLQ
401 ----- 450
us-09-873-409-5 RLYDPDDGFI WVDENDIRAL NVRHYRDHIG VVSOEPVLFG TTISNNIKYG
451 ----- 500
us-09-873-409-2 RDDVTDEBEM RAAREANAYD FIMEPPNKEN TLVGEKGAQM SGGQOKORIAI
501 ----- 550
us-09-873-409-5 ARLALVNPKI LILDEATSL DSEKSAVOA ALEKASKGRT TIVVAHRLST
551 ----- 600
us-09-873-409-2 IRADADILVTL KDGMLAEKGA HAEIMAKRGL YVSLVMSODI KKADEQMESM
601 ----- 650
us-09-873-409-5 TYSTERKTNS LPLHSVYSIK SDPIDKAES TOSKEISLPR VSLIKLIKLN
651 ----- 700
us-09-873-409-2 KPEMPFVLUG TLASVINGTV HPVSIIPAK IITMFGNNDK TLUKHDAEY
701 ----- 750
us-09-873-409-5 SMIFVILGVI CFVSYFMOGL FYGRAGEILT MRLRLHAFKA MLYQDIAMPD
750 -----

```

```

us-09-873-409-5 SMIFVILGVI CFVSYFMOGL FYGRAGEILT MRLRLHAFKA MLYQDIAMPD
751 ----- 800
us-09-873-409-2 EKENSTGGLT TLIAIDIAOI QGATGRIGV LTQATNMGL SVIISFIYGM
801 ----- 850
us-09-873-409-5 EKENSTGGLT TLIAIDIAOI QGATGRIGV LTQATNMGL SVIISFIYGM
851 ----- 900
us-09-873-409-2 TIVSLTRERA PEQYTEMLQ TOHNTSKKA QIIGSCYAFS HAFIYFAYVA
901 ----- 950
us-09-873-409-5 GFRFGAYLLO AGRTMPEGMF IVFTAIAYGA MAIGKTLVLA PRYSKAKGA
951 ----- 1000
us-09-873-409-2 AHLFALLEKK PUIDRSQBG KKPDTCEGNTL EPREVSFPYP CRPDVPIILRG
1001 ----- 1050
us-09-873-409-5 LSLISIRGKT VAFVSSGCG KSTSVOLLQOR LYDPVOGQVL PDGVDAKEIN
1051 ----- 1100
us-09-873-409-2 VQMLRSQIAI VPOEVLPRNC SIENIAYGD NSRVVPLDEI KEAANANAH
1101 ----- 1150
us-09-873-409-5 SPIEGLPERY NTQVGLKGAQ LSGQOKORIA IARALLQPK IILLDEATSA
1151 ----- 1200
us-09-873-409-2 LNDSEKVVQ HALDKARTGR TCVLVTHRLS AIONADLIIV LHNKIKKEQG
1201 ----- 1222
us-09-873-409-5 THQELLNRND IYFKLVNAOS VO
1222 -----

```

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GAP of: us-09-873-409-2 check: 7710 from: 1 to: 812

FROMIG of: /staff/overflow/sdavid-tmp/dectemp/yu409/US09873409.pep  
sequence 2, application us/09873409

general information:

applicant: frank, markus

applicant: sayegh, mohamed

title of invention: a gene encoding a multidrug resistance human  
p-glycoprotein

to: us-09-873-409-5 check: 6997 from: 1 to: 1222

FROMIG of: /staff/overflow/sdavid-tmp/dectemp/yu409/US09873409.pep  
sequence 5, application us/09873409

general information:

applicant: frank, markus

applicant: sayegh, mohamed

title of invention: a gene encoding a multidrug resistance human  
p-glycoprotein

Symbol comparison table: /SIDS/appl/gcg/gcgcore/data/rundata/biosum62.cmp  
Compcheck: 1102

Gap Weight: 8 Average Match: 2.778  
Length Weight: 0 Average Mismatch: -2.248

Quality: 4079 Length: 1222

Ratio: 5.023 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

Match display thresholds for the alignment(s):

= 2  
= 1

us-09-873-409-2 x us-09-873-409-5 December 17, 2003 13:39

```

1 .....MVDENDIRALNVRHYRDHIGVVSQEPVLFGTTSNNIKYG 40
  |||||
401 RLVDPDGPIVVDENDIRALNVRHYRDHIGVVSQEPVLFGTTSNNIKYG 450
  |||||
41 RDDVTDEMERARARANA YDFIMEFPNKFNTLVGEKGAQMSGGQKORIAI 90
  |||||
451 RDDVTDEMERARARANA YDFIMEFPNKFNTLVGEKGAQMSGGQKORIAI 500
  |||||
91 ARAVVRNPKIILDEATSAIDSEKSAVOALAEKSKGRTTIVVAHRLST 140
  |||||
501 ARAVVRNPKIILDEATSAIDSEKSAVOALAEKSKGRTTIVVAHRLST 550
  |||||
141 IRSADLIYTLVDGMLAEKGAHAELMAKRGILYSLVMSODIKKADROMESM 190
  |||||
551 IRSADLIYTLVDGMLAEKGAHAELMAKRGILYSLVMSODIKKADROMESM 600
  |||||
191 TYSTERKTNLSPLHSVKSIKSDPIDKAEESTOSKEISLPEVSLKILKLN 240
  |||||
601 TYSTERKTNLSPLHSVKSIKSDPIDKAEESTOSKEISLPEVSLKILKLN 650
  |||||
241 KPEMPFVLGTLASVLTNGTVHPVPSIIPAKIITMFGNNDKTKLKHDAEIT 290
  |||||
651 KPEMPFVLGTLASVLTNGTVHPVPSIIPAKIITMFGNNDKTKLKHDAEIT 700
  |||||
291 SMIFVLIGVICFVSYFMQGLFYGRAGBILTMRLRLAFKAMLYODIAMPD 340
  |||||
701 SMIFVLIGVICFVSYFMQGLFYGRAGBILTMRLRLAFKAMLYODIAMPD 750
  |||||
341 EKENSTGGLTTLTILADIAIOIGATGSRIGVLTONTATNMGLSVIISFIYGM 390
  |||||
751 EKENSTGGLTTLTILADIAIOIGATGSRIGVLTONTATNMGLSVIISFIYGM 800
  |||||

```

```

391 EMTFLILSIAPVLAVTGMIETPAATGFPANKOKOELKAKGIATALEENIR 440
  |||||
801 EMTFLILSIAPVLAVTGMIETPAATGFPANKOKOELKAKGIATALEENIR 850
  |||||
441 TIVSLTRKAEQMYEEMLTQOHNNTSKAQIIGSCYAFSAFTYFAYAA 490
  |||||
851 TIVSLTRKAEQMYEEMLTQOHNNTSKAQIIGSCYAFSAFTYFAYAA 900
  |||||
491 GFRFGAYLIQGRMTPEGMPIVFTAIAYGMAIGKTVLAEYSKASGA 540
  |||||
901 GFRFGAYLIQGRMTPEGMPIVFTAIAYGMAIGKTVLAEYSKASGA 950
  |||||
541 AHLPALEKKNIDRSQEGKPDTCGNLEFRFVSFPYPCRPDVFILRG 590
  |||||
951 AHLPALEKKNIDRSQEGKPDTCGNLEFRFVSFPYPCRPDVFILRG 1000
  |||||
591 LLSIIEKGTVAFYSSGCGKSTSVQLLQRLYDPVQGVLPDGVDAKELN 640
  |||||
1001 LLSIIEKGTVAFYSSGCGKSTSVQLLQRLYDPVQGVLPDGVDAKELN 1050
  |||||
641 VQWLRSGQAIYPOBPVLFNCSIAENIAYGDSRVVPLDEIKKANANNTI 690
  |||||
1051 VQWLRSGQAIYPOBPVLFNCSIAENIAYGDSRVVPLDEIKKANANNTI 1100
  |||||
691 SFISGLPEKNTVOGLKGAQSLSGGOKORLAIRALLOPKILLDEATSA 740
  |||||
1101 SFISGLPEKNTVOGLKGAQSLSGGOKORLAIRALLOPKILLDEATSA 1150
  |||||
741 LDNDEKVVQHALDKARTGRCLVYTHRLSAIQNADLIIVLHNGKIXEKG 790
  |||||
1151 LDNDEKVVQHALDKARTGRCLVYTHRLSAIQNADLIIVLHNGKIXEKG 1200
  |||||
791 THOBLRNNDIYFPLVNAQSVQ 812
  |||||
1201 THOBLRNNDIYFPLVNAQSVQ 1222
  |||||

```

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OW protein - nucleic search, using frame\_plus\_p2n model

Run on: December 17, 2003, 14:41:08 / Search time 83 Seconds

(without alignments)  
2.344 Million cell updates/sec

Title: us-09-873-409-5

Sequence: 1 MIIIGIIASLVNGACPLPLMP.....QELLRNRDIYFKLVNAQSVQ 1222

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1 segs, 79611 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seg length: 0  
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 1 summaries

Command line parameters:

-MODE=frame+p2n.model -DRV=soft -Q=us-09-873-409-5 -DB=2341014\_1997  
-SUFFIX=pic -OUT=align5\_1997 -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits  
-START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCALLIGN=200  
-THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pic  
-NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6 -NO\_XLPHY  
-NGG\_SCORES=0 -LONGLOG -THRAD=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7  
-Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database: 2341014\_1997:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	932	15.1	79611	1	AC002486 ACCESSION:AC002486

#### ALIGNMENTS

RESULT 1  
AC002486 79611 bp DNA linear PRI 22-AUG-1997  
LOCUS Human BAC clone RG367017 from 7p15-p21, complete sequence.  
DEFINITION AC002486  
ACCESSION AC002486  
VERSION AC002486.1 GI:2341014  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 79611)  
AUTHORS Kalicki, J., Smith, A. and Gibson, A.  
TITLE The sequence of H. sapiens BAC clone RG367017  
JOURNAL Unpublished (1997)  
REFERENCE 2 (bases 1 to 79611)

AUTHORS  
TITLE  
JOURNAL  
COMMENT

#### COMMENT

Waterston, R.  
Direct Submission  
Submitted (22-AUG-1997) Department of Genetics, Washington  
University 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
SUBMITTED BY:  
Genome Sequencing Center  
Department of Genetics  
Washington University  
St. Louis MO 63108, USA  
http://genome.wustl.edu/gsc  
mailto:sapiens@wustl.wustl.edu

NOTICE: This sequence may not represent the entire insert of this  
clone. It may be shorter because we only sequence overlapping  
clone sections once, or longer because we provide a small overlap  
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
all regions were double stranded or sequenced with an alternate  
chemistry; an attempt was made to resolve all sequencing problems,  
such as compressions and repeats; all regions were covered by  
sequence from more than one subclone; and the assembly was  
confirmed by restriction digest.

#### MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and  
sequencing collaboration between the NHGRI Chromosome 7 Mapping  
Project (Eric D. Green, Director), John D. McPherson in the  
Department of Genetics (Washington University), and the Washington  
University Genome Sequencing Center. For additional information  
about the map position of this sequence, see  
http://www.nhgri.nih.gov/DIR/GTB/CHR7 or send  
mailto:egreen@nhgri.nih.gov

#### SOURCE INFORMATION:

This clone is from a release of the human BAC library. The library  
contains cloned DNA from human sperm. See: Shizuya et al., Proc.  
Natl. Acad. Sci. USA 89:8794-7 (1992); Kim et al., Genomics  
34:213-8 (1996). The clone is available from Research Genetics,  
Inc. (http://www.reggen.com).  
VECTOR: pBelOBAC11  
Selection: chloramphenicol

#### NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RG086D03. The actual start of  
this clone is at base position 1 of RG367017. This clone is part of  
an unanchored island, orientation is unknown.

This clone contains STS SMS51805 (NID:G1113222).

#### FEATURES

FEATURES	Location/Qualifiers
Source	1..79611 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="7" /map="7p15-p21" /clone="RG367017" /clone_lib="CITB-HS-A" 683..715 /rpt_family="L1" 1781..2410 /rpt_family="L1" 3374..3875 /note="probable rae-related (RAI) pseudogene, similar to (PID:G1346952)" 3429..3529 /note="similar to EST T29472 (NID:G611570)" 3550..3804 /note="similar to EST AA523370 (NID:G2264082) nt67d09.s1" 3810..4260 /note="similar to EST AA403045 (NID:G2055607) zv63c09.r1" 3903..4207 /note="similar to EST Z44835 (NID:G574005)"
repeat_region	1781..2410
misc_feature	3374..3875
misc_feature	3429..3529
misc_feature	3550..3804
misc_feature	3810..4260
misc_feature	3903..4207

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misc_feature      complement(3910..4337)
                   /note="similar to EST N62870 (NID:g1210699) y283e03.b1"
misc_feature      4025..4431
                   /note="similar to EST T74360 (NID:g691035) yc8h10.r1"
misc_feature      4217..4745
                   /note="similar to EST AA449169 (NID:g2162632) zx02g12.r1"
misc_feature      4265..4572
                   /note="similar to EST F12824 (NID:g708845) "
misc_feature      complement(4459..4724)
                   /note="similar to EST AA382990 (NID:g2055360) "
misc_feature      4546..4861
                   /note="similar to EST AA296743 (NID:g1949076) "
misc_feature      complement(4639..4792)
                   /note="similar to EST AA368261 (NID:g2020654) "
misc_feature      4733..4933
                   /note="similar to EST AA447258 (NID:g2159923) zw93e03.r1"
misc_feature      4938..5215
                   /note="similar to EST AA447258 (NID:g2159923) zw93e03.r1"
misc_feature      complement(5063..5638)
                   /note="similar to EST AA044672 (NID:g1522874) zk73a09.b1"
misc_feature      complement(5068..5638)
                   /note="similar to EST AA044672 (NID:g1522874) zk73a09.b1"
misc_feature      5145..5435
                   /note="similar to EST H97948 (NID:g1118833) yx04e05.b1"
misc_feature      5147..5571
                   /note="similar to EST W56187 (NID:g1358144) zdl4c10.r1"
misc_feature      complement(5642..5673)
                   /rpt_family="L1"
repeat_region     5782..6074
                   /rpt_family="ALU"
repeat_region     6499..6859
                   /rpt_family="L1"
repeat_region     9618..9657
                   /rpt_family="L1"
repeat_region     complement(10090..10285)
                   /rpt_family="L1"
repeat_region     13808..13899
                   /rpt_family="L1"
repeat_region     complement(16807..16844)
                   /rpt_family="L1"
repeat_region     complement(18057..18887)
                   /rpt_family="L1"
repeat_region     18866..20301
                   /rpt_family="L1"
repeat_region     complement(19766..19812)
                   /rpt_family="L1"
repeat_region     complement(20583..20874)
                   /rpt_family="ALU"
repeat_region     complement(21847..22287)
                   /rpt_family="L1"
repeat_region     21868..22285
                   /rpt_family="L1"
repeat_region     complement(22880..22983)
                   /rpt_family="ALU"
repeat_region     23346..23476
                   /rpt_family="L1"
repeat_region     23578..24277
                   /rpt_family="L1"
repeat_region     24960..25002
                   /rpt_family="L1"
repeat_region     25076..25163
                   /rpt_family="L1"
repeat_region     25210..25280
                   /rpt_family="L1"
repeat_region     25304..25362
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repeat_region     25420..25459
                   /rpt_family="L1"
repeat_region     25485..25965
                   /rpt_family="L1"
repeat_region     25968..26249
                   /rpt_family="ALU"
repeat_region     26287..26341

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repeat_region     /rpt_family="ALU"
repeat_region     26702..27088
                   /rpt_family="L1"
repeat_region     27089..27207
                   /rpt_family="ALU"
repeat_region     27223..27260
                   /rpt_family="ALU"
repeat_region     27261..28126
                   /rpt_family="L1"
repeat_region     complement(29836..30118)
                   /rpt_family="ALU"
repeat_region     complement(31821..32163)
                   /rpt_family="L1"
repeat_region     complement(32179..32565)
                   /rpt_family="L1"
repeat_region     complement(32566..32857)
                   /rpt_family="ALU"
repeat_region     complement(32858..33932)
                   /rpt_family="L1"
repeat_region     33937..35195
                   /rpt_family="L1"
repeat_region     36415..36448
                   /rpt_family="L1"
repeat_region     39372..40123
                   /rpt_family="L1"
repeat_region     40278..40297
                   /rpt_family="L1"
repeat_region     41686..41708
                   /rpt_family="L1"
repeat_region     complement(41775..42243)
                   /rpt_family="L1"
repeat_region     43264..43555
                   /rpt_family="ALU"
repeat_region     complement(45048..45074)
                   /rpt_family="L1"
repeat_region     45325..45368
                   /rpt_family="L1"
repeat_region     46217..46780
                   /rpt_family="L1"
repeat_region     complement(47281..47600)

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```

Alignment Scores:
Pred. No.:      0
Score:          932.00
Percent Similarity: 23.51%
Best Local Similarity: 19.32%
Query Match:    15.13%
DB:             1
                Gaps: 41

```

```

us-09-873-409-5 (1-1222) x ACC002486 (1-79611)

```

```

QY      33 CysLeuValGlnThrSerPheArgLeuThrLeuTyrrValGlylle 52
DB      56932 TGGCTTCAGTCTCAATTCCTTCCTTCAGGTTGACCTGATATATGTTGAAATA 56991
QY      53 G1VValAlaAlaLeuIlePheGlyrrIleGlnIleSerLeuThrIleIleThrAlaIa 72
DB      56992 GGTGTGCTGCTTGAATTTTGTATACATACAGATTTCTTGAGATTAATACGACGA 57051
QY      73 ArgGlnThrLysArgIleArgLysGlnPhePheIleSerValIleuAlaGlnAspIleGly 92
DB      57052 CGACAGACCAAGAGATTCGAAAACAGTTTTCATTCAGTTTGGCACAGACATCGGC 57111
QY      93 TrpPheAspSerCysAspIleGlyIleuAsnThrArgMetThr----- 107
DB      57112 TGGTTTGATAGCTGTACATCGGTGAATTAACATCGCATGACAGATGAAGAGATGAT 57171
QY      107 ----- 107
DB      57172 ATTGTAGTACGTTAGCTTGTCTTCATPANGTCAGATGAATGACCTAATCACTTATTT 57231
QY      108 -----AspIleAspLysIleSerAspGlyIleGlyAspLysIleAlaLeuLe 123

```











GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: December 17, 2003, 15:11:26 / Search time 129 Seconds  
(without alignments)  
2.277 Million cell updates/sec

Title: us-09-873-409-5  
Perfect score: 6159  
Sequence: 1 MIIIGIIASIVNGACPLPLML.....QELLRARDYFKLVNAGSVQ 1222

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.1  
Ygapop 10.0, Ygapext 0.1  
Fgapop 6.0, Fgapext 0.1  
Delop 6.0, Delext 0.1

Searched: 1 segs, 120169 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seg length: 0  
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1 summaries

Command line parameters:  
-MODE=frame\_plus.p2n.model -DRV=soft -Q=us-09-873-409-5 -DB=4827303\_1999  
-SUFFIX=pro -OUT=align5\_1999 -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits  
-START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCALIGN=200  
-THR\_SCORE=pcr -THR\_MAX=100 -THR\_MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pcr  
-NORM=ext -HEADSIZE=500 -MCLEN=0 -MAXLEN=2000000000 -NCPU=6 -NO\_XLPXY  
-NEG\_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6  
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database: 4827303\_1999:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	1739.47	28.2	120169	1	AC005060 ACCESSION:AC005060

## ALIGNMENTS

RESULT 1  
AC005060/c 120169 bp DNA linear PRI 14-MAY-1999  
LOCUS AC005060 Homo sapiens clone RG086D03, complete sequence.  
DEFINITION AC005060  
ACCESSION AC005060  
VERSION AC005060.2 GI:4827303  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 120169)  
Waterston,R.H.  
TITLE The sequence of Homo sapiens clone  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 120169)

AUTHORS Waterston,R.H.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-1998) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
3 (bases 1 to 120169)  
REFERENCE Waterston,R.H.  
AUTHORS Direct Submission  
JOURNAL Submitted (14-MAY-1999) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
[WARNING] On Oct 2, 2000 this sequence was replaced by a newer  
version g1:10445386.  
COMMENT On May 14, 1999 this sequence version replaced g1:3212931.  
FEATURES  
Source 1..120169  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="RG086D03"

Alignment Scores:  
Pred. No.: 0 Length: 120169  
Score: 1739.47 Matches: 838  
Percent Similarity: 6.47% Conservative: 155  
Best Local Similarity: 5.46% Mismatches: 227  
Query Match: 28.24% Indels: 14147  
DB: 1 Gaps: 20

us-09-873-409-5 (1-1222) x AC005060 (1-120169)

Qy	1	MetIleu-----	-----GlyIleu-----	Ala 7
Db	70326	ATATCTCTAGTTCACGCACTCAACTCTTGAGGCTGAAGGATGCTCCACTCAGCC		70267
Qy	8	SerLeuValAsnGlyAla---CysLeuProleu-----		17
Db	70266	TCCCAAGTACGCGGAACAGGCGCAGCAGCAGCTGCTGCTGCTAATTTTTCATTTTATG		70207
Qy	17	-----		17
Db	70206	TAGAGACAGAGCTTCGATGCTGCTAGGCTGCTGTAACCTCGGCTCAAGTATC		70147
Qy	18	MetProleu-----ValleuGly-----		23
Db	70146	CTCCCACTTGCGGCTCCCAAGTGTGAGATTATTAAGTAGCCACCCGACCGCTTA		70087
Qy	24	-----		Glu 24
Db	70086	GAGCAGCTATATCTTTTCTTTTGTGAGACAGTCTCTCTGTCCACCCAGGCTGAG		70027
Qy	25	MetSerAspAsnLeuIleSerGlyCys-----		33
Db	70026	TGCAGTGGCAGATCTCATCTCAGTCAACCTCCGCTCCGGGTTCAAGCAGCTCTCT		69967
Qy	33	-----		33
Db	69966	GCCTCAGCTCTCAATTAGCTGGAGCTACAGAGTCCACCAACGACCCAGCTAATTTT		69907
Qy	34	-----LeuValGlnThr-----		37
Db	69906	GATATTTTATAGTAGAGCGGGCTTTCACACAGTTGTGACAGCTGTATCCAACTCTGACC		69847
Qy	37	-----		37
Db	69846	TCTGTGATCTTCCTCCACTCGGCTGTAAATCCAAAGCTCGGATTAACAGGTGAGCC		69787
Qy	37	-----		37
Db	69786	ACCGTCCAGCTGAATCTAATCTTTAAAGTTAATAGAACACAAACAGAGGTAGT		69727
Qy	37	-----		37

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Db 69726 GAGGATCAGGACATATATATGTTACTAATAGAGATATCCAAAGAAAAGATAA 69667
QY 37 -----
Db 69666 CTGCCAGTGGATATGTTTATCTTCGACAAATATAGATCTGTGCCAAGATTGAA 69607
QY 37 -----
Db 69606 TCCAAAAAAGTAAATCATCTGGCTTCAAAATATTTAAAGAACTTCCAGTGGAAATTA 69547
QY 37 -----
Db 69546 ATACATGATACAGGTCTACAAAACATACCCCTATCAAGTAATGATGACAAGTAAT 69487
QY 37 -----
Db 69486 CTGTATATATTTAGATTAATAATTTATATTTAAAGAACATGAAATCTTATTTCTC 69427
QY 38 ---AanThr---TyrSerPhe-----PheArgLeuThrLeuTyr-- 48
69426 AACACACATATATATATTTTAAATAATAGCTCCATGATGACATGACATCATATATAT 69367
QY 49 ---TyrValGlyIleGlyValAlaAlaLeuIlePheGly----- 60
69366 AATTTTATGATGCTATAGAGACATTTAGTATTTTATGAGAGACCTTCCAGAACCA 69307
QY 61 -----Tyr----- 61
69306 GGGCAAAAGCAATTTTTTTTTTTTATTTATGACCCAGATTTTAAACAGTACTTATGGA 69247
QY 61 ----- 61
69246 CATTTTAAGGATTAACCAAAAGCATTCATATAGTTTTCATGACACACTTATATGC 69187
QY 61 ----- 61
69186 ATTAATTAACATTAAGATGATTTGGGACATGATTTCAATCAAAAGACATAGTAA 69127
QY 61 ----- 61
69126 GGAGAGAAATGGGCTGGAAAAGAGAAAGTATTTCTTAAGTCACTTACAGTAAG 69067
QY 61 ----- 61
69066 AAAAGCAAAATTTGAAAACAGAGAGCCCTTGTCATTTCCCTAGAAAGAACTGGACA 69007
QY 61 ----- 61
69006 ATCTAGAGATTCATTCAGAAAAGCAAGTGGTGAAGGCTGACCTTACAGCTGTAGC 68947
QY 62 -IleGlnIleSerLeu----- 66
68946 AATACAGCTTTCCTTAGAAATTTCTTAAGCGTCCGAAACCCAGCGCAGCCTTAGGGAAT 68887
QY 66 ----- 66
68886 CTCCTTTCGCATCTACTCATTCCTCCAGCATCTCTCCAGTCCCAAGGCTTAGATGCC 68827
QY 66 ----- 66
68826 CAACACCTACCGCAAAAGCCAGGCTTACAGACATTAACCGACGTGAAGCCACACTC 68767
QY 66 ----- 66
68766 CAGACTGCTTCTCCATCTGAGCTTGAGATGACCCCGCACAGAGCATTTAGTATTTA 68707
QY 66 ----- 66
68706 AGGAAAGCATGGAAGGCTCCAAACATGCCAAAGAACTTAAGTTCACAGATCTCACCG 68647
QY 67 -----Tyr----- 67
68646 GTTGTATAGTCCATATGACTGTGAAACTTATGTTGGGGGGTGGAGAGGACAGAGCAAG 68587

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QY 68 -----IleIleThrAlaAlaArg-----GlnThrIysArgIleArg 79
Db 68586 ACAGTGTGTAG--TCACTCTGGGCTTCCATTAACAAAGACCAACAGCTGAGGCTGCA 68529
QY 79 GlyGlnPhePheHisSer-----ValLeu-----AlaGlnAsp----- 90
Db 68528 ACAACAGACATTCATTTCTTACAGTTCTTGAAAGCTAGAACCCCAAGAACAGATGTCG 68469
QY 91 ---IleGly-----TyrPheAspSer-Cys----- 97
Db 68468 CAGATTTGGGTTTATCTCCAGAGGCGCTTGGCTTGTAGTGGCTGTCTTATACGCTTC 68409
QY 97 ----- 97
Db 68408 ACAGATCTTCTCTGTATGACAGTGTCTGTGTCAGATTTCTTTTCTTTT 68349
QY 98 -----Asp-----I 99
Db 68348 TTTTCTTTTGAACAGACTTTTGTCTGTCTCCAGGCTGACAGTGGCGTTATG 68289
QY 99 IeGlyGlnLeu-AenThrArgMet----- 106
Db 68288 TTGGCTCAGTGCACACCTCCGCTCCGCGGTTCAAGGATTCCTGCTCAGCGCTCGA 68229
QY 107 -----ThrAsp----- 108
Db 68228 GTACCTGGATTTACAGACAGCACACACATGCCCGGCTAATTTTATTTAGTAGAGATGA 68169
QY 109 -----IleAspLys-----IleSerAspGly-----IleG 117
Db 68168 GGTTTACCATGTGTATTAAGCTGTGTCTGACATCTCGACCTCATGATCTGCCGCTCG 68109
QY 117 Iy--AspLysIleAlaLeu-----PheGlnAsn 126
Db 68108 GCCTCCCAAGGTCTGGATTTACAGGCGCAGCCAGCCAGCTGGCCCAATTTCTCTT 68049
QY 127 MetSerThrPheSerIleGlyLeuAlaValAlaGlyLeu-ValIysGlyTyrIysLeuThr-- 145
Db 68048 CTTAACAAGATATATATATACAGTTAAGTTCAGCTTAACTTCACTTAACCTTA 67989
QY 146 -----LeuValThrIleSer----- 150
Db 67988 ATTATCCGTATCTATATATTTATTTATTTATTAATTAACCTTATCTCAAAATACGTAACA 67929
QY 151 -----TherSer 153
Db 67928 TTCTGTACATTCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTATACAGAGC 67869
QY 153 roleuIleMetAla-----SerAlaAlaIaCysSerArgMetValIleSerLeuTh 170
Db 67868 CTGCTCTGTGCGCCAGGCTGAGTGCAGTGGCGCAATCTCGCTCATTTCCAAAGCTCCAC 67809
QY 170 rSerLysGlnLeuSerAlaIySer-----LysAlaGlyYA 182
Db 67808 CTCGCC--GAGTTAACGCATTTCTCTGCGCTCAGCGCTCGTAGTGTGGAGCTACAGGCG 67751
QY 182 Ia-----ValAlaGlu----- 185
Db 67750 CCGGCACACAGCGCTGCTAATTTTTTGTGTTTTTTTTTTTTTTTATAGAGACGGGTTTC 67691
QY 186 GluValIleSer-----SerIleArgThr----- 193
Db 67690 ACCGTGTACAGAGATGCTCTTGATCTCCGACCTCGTAGACAGCCCGGCTGCGCTCC 67631
QY 194 -----ValIleAlaPheArgAla----- 199
Db 67630 CAAGTCTCGTGAATTCAGCGCGTAGAGCCAGCGGCGCTGSCCAATACATACTATCTG 67571
QY 200 -----GlnGlnLysGlnLeu-----GlnArg----- 206
Db 67570 ATAACTGAGAGTTAGACTTAACATATATATATAGTGGGTGAGGAGACAAATGTAGCTT 67511

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QY 207 -----SerPheLeuAenIleThrArg----- 214
DB 67510 ATAAATACATACCATTTATCTCTTTATCCTTAACTCC-AGGGAGATGAAGTAAAG 67452
QY 215 -----TyrAla----- 219
DB 67451 TCAGCATTTATATGCGAAATGCAATCCCATTTAGGCCCATGGTTCTTAGAGTTAGTAT 67392
QY 220 -----PhePro----- 223
DB 67391 CATACCTTTAAACCTTAAACGAGCTACCTTGCTCATCTTAGTTTTCAGATTTCAAGT 67332
QY 224 -----LeuLeuSerCysValLeu**PheVal----- 232
DB 67331 TTTTGAAGTGTGCTGTGTGTGTGTATTTTAACTTTTGAAATTTCTTAGAGTTTAACT 67272
QY 233 -----ArgTyrThrGlnAsnLeuIleAspAlaVal 242
DB 67271 GAGAAATTGAAAAATGTTGAGTCATCACAGATACAGTCTTGAAACTGAAACCAAGAG 67212
QY 243 AspPhe-GlyIleIys-ArgThrIleAlaSerIleValSerLeu-----Gly----- 257
DB 67211 TTTTTAGAATTAGGACAGAGCCCTGGGAGGAGAGATTTGTATGTTATTTTAA 67152
QY 257 ----- 257
DB 67151 ATGAAGATGCTAATTTTATATAGTTGGTGAATAATGATGTAATCTTTAGAGAACAA 67092
QY 258 -----AlaValTyrPhePheMetAsnGlyThrTyrGly 268
DB 67091 TTTCGCAATACCATCAAGAAATGTAAGATATATACACCTTTTAAATTTCTTCAAGGT 67032
QY 269 Leu--AlaPheTyrGly-----ThrSerLeuIle-----LeuAsnGly 281
DB 67031 TTATAACCTGTATCATTAATCATTTATTTGACTCAAAATTTATCCAGATTCAGCCAGTGG 66972
QY 281 yGluPro-----GlyTyrThrIle--GlyThrVal----- 290
DB 66971 AAGTCCCTTCAGATGGGAGAAATTACACCTTTAAGGTGAATTCAGATTAAGAAATTTAA 66912
QY 291 -----LeuAlaVal-----PhePhe----- 295
DB 66911 CATAGGCAATTTGAGGTGAAGGTGAATGAGAACAAAGATTTTTCACAAAGATGT 66852
QY 295 ----- 295
DB 66851 TCATTAATCTTATTTTATTAATACGAAGCAACCAATGAGGCAACCCAAATATTT 66792
QY 296 -----SerValIleHis-----SerSerTyr----- 302
DB 66791 TTGGAGAAATTTTAATTAATCTGAGTAAATGTAACAGAAATTAATCAGATACAAACTG 66732
QY 303 -----CysIleGlyAlaAlaVal----- 308
DB 66731 CATGACATTAATAACCAATCTGAATGTATTAAGTATTTATGCTAGAGAGATAGAG 66672
QY 309 -----Pro-----His----- 310
DB 66671 TTTTAATCTTATCTAAGCTTTTCTAATGATCTGTTTTCATGATCAGAGCAAAAAATAT 66612
QY 311 -PheGluThr-----PheAlaIleAlaArgIleAlaPhe----- 322
DB 66611 ATTTCAACCTGAGTCAATTCGTCTTTCAGGTAAATAGGGGCTCATTTTTTTAA 66552
QY 323 -----His-----IlePheGlnValIle-----AspIle 330
DB 66551 TCCCAACATCAAAAGAACTTATATGTTTCAGCTTATCTTAAGTATCATATCACCAGCTGA 66492
QY 330 GlySerProSerIleAspAsnPhe-----SerThrAlaGlyTyrIleProGluSerIleGluG 349
DB 66491 AAGATGATCATTA--AATGTGTAGTTCTTATTAAGTTATTAAGTTAATCTTACATATTT 66434
QY 349 IyThrValGluPheIysAsnValSerPhe-AsnTyrProSerArgPro--SerIleIysI 368

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DB 66433 TGAAGTAT--TTTAAAAATTTATTTTACTATACT--ATGACTCCTTTCTATCTTGA 66378
QY 368 Ie-----LeuIlySerGlyLeu-----AsnLeu--ArgIleIysSerGly----- 379
DB 66377 TATTGCTCTTGTAGATCTTACTAGAGTAAACCAATTTATATGTGCAAAAAATGGGAGTGA 66318
QY 380 -----GluThrValAla-----LeuValGlyLeuAsnGly 389
DB 66317 GAGAAATGCTATCCAAAGATATACCTTTATATGATATATCATATATCTTCACTCAACT 66258
QY 390 -----SerGlyIysSer-----ThrVal-----ValGlnLeu 398
DB 66257 ACTATGATAGAGTGTGAGTGAAGTGTGCTGGCTTCCTGCAAGTGTGGAAAGGGGTAGGGCTG 66198
QY 399 -----LeuGln--ArgLeuTyrAsp----- 404
DB 66197 GGGTTTGAGCCCGCATATATATGACACCCAGTGTGGAGCCCGGTGACAGGAAGCAG 66138
QY 405 --ProAspAspGly-----PheIleMetValAspGlu--AsnAspIleArgAla 419
DB 66137 AGCCAGAGCAGGTGAGAGAGGTGTTCTGACAG--GAAAGAGCAGAGACATGAGAGCA 66080
QY 420 LeuAsnValArgHisTyrArgAsp-----HisIle----- 429
DB 66079 GA-TGGGTACCATGAG--AGAGATTAATCATATGATCAATCTATTAAGACATGGAG 66022
QY 430 -----GlyValValSerGlnGlu----- 435
DB 66021 CCAATTTCTCCTTGTGAAAGAGGGGTATTAACAATATGAAAGAGAAACCTGGAAT 65962
QY 435 ----- 435
DB 65961 AACCTTAATGTTGAATTTGGAATGAGAGTATGATATGACTCATGAGTTTCAAGAAAT 65902
QY 435 ----- 435
DB 65901 ATACGAAACAAATATATGATGTAATGTGTGTTGTAATCAATCAATACACACACACAC 65842
QY 436 -----Pro-----ValLeuPheGlyThr-- 441
DB 65841 ACACACACACACACACATTTCTAGTCTGACCACTGAATTTCTAGTAAATATGATGATCAAC 65782
QY 442 -----ThrIleSer-----AsnAsnIle----- 447
DB 65781 CAGCACATATCTTGAATCTGCTAATTAATTAATTTCTCACTAAAGAACCCAGGATCTTGG 65722
QY 448 -----LysTyrGlyArgAsp----- 452
DB 65721 AGAATGACTAATTCGAAAGATGAGGACAGACAGATGACAGATGAATGAAATCATTT 65662
QY 453 -----AspVal-----ThrAspGluMetGluArg--Ala 463
DB 65661 TTGTGTGAGAAATGAGACATATTCAAAACCTGATAGTATATGCAAGACAAAGCC 65602
QY 463 IAspGluAla-----AsnAlaTyr 469
DB 65601 AACGTGAAGGACTTCACGTGCTACATCTGGATTAATTTAGTCAAAATTAATGATATAT 65542
QY 470 Asp-----PheIleMetGlu----- 474
DB 65541 AGTAACAGTTTAAACAATGAAATTTAAAGTCAATTAGTTCTATCTACATTAAT 65482
QY 475 -----PheProAsnIys-----PheAsnThrIle 482
DB 65481 AAGTTGAAGATTGATGAGAAATTTGAGATTTGACATAGCTTCAAGTCTTCAAGACATTT 65422
QY 482 uValGlyGlyIysGly-----AlaGlnMetSerGlyGlyGln-----LysGlnArgIle 499
DB 65421 TATTAATTAACAAAGGAGAAACACATTCATACGCGAGAAACCTGGAAGAACCATCT 65362
QY 499 IAlIAlaArgAlaLeuValArgAsn-----Pro-----LysIle-LeuIleI 513

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Db 65361 TAATTA- TTATTACAAGTGAACATGCTGAAATGGAGCAATCAAAATCGGTGCAC 65303  
 Qy 513 euAEP-- GluA1-----ThrsrAlaLeu-----Apsr-----GluSer 524  
 Db 65302 TTAATGAGATGATGAGAAAGAACACAGCATCTTCTTAAGATGATATTTGAATCT 65243  
 Qy 525 -----LysrAlaValAlaAlaLeuGluLeu----- 534  
 Db 65242 AATTGAGAGAAATATGAGATTA--GCTAAATTTGAGAAATTTCTACAGATATCTGGCT 65185  
 Qy 535 -----AlaSerLysGlyAlaThr--ThrIle-----Val 543  
 Db 65184 CGCGATCTCAAAAGTCAAGGTCAATGACATCAAGTAAATGAAGAGCCAGCGCG 65125  
 Qy 543 ValAlaHisAlaLeu-----SerThrIle-----Argse 553  
 Db 65124 GGTGGCTCAGCGCTGTATCCGACAGAGTTGGAGGCGGAGCGGCGATCAGAGGTC 65065  
 Qy 553 rAlaAsp-----LeuIleValThrLeuLeu----- 561  
 Db 65064 AGGAGATCGAGACCATCTGGCTTAACAGGTGAACCCCGTCTCTACTAAATACAAA 65005  
 Qy 562 -----AerGlyMetLeu-----AlaGlyLysGly 569  
 Db 65004 ATTACCGGCGATGTGTGCGCGCTGTATGCCAGCTACAGCGGAGGCTGAGCGAGA 64945  
 Qy 570 -----AlaHisAlaGluLeuMetAlaLysArgGly-----LeuTyrTyr 582  
 Db 64944 GAATGGCGGTAAACCCGAGGCGGAGGCTTGCAGTGAGATCGGCGCATCTGCC 64885  
 Qy 583 SerLeu-----ValMetSerGlnAspIleLysLysAlaAspGluGlnMetG 598  
 Db 64884 AGCTGGGGCGACAGAGGAAACTGTGCTCAAAAAAAGGATGA 64825  
 Qy 598 LysMetThrTyrSerThrGluArgLysThr-----AspSer----- 610  
 Db 64824 AGAAT-----TATTCATATTAAGAGAGACTAAAGAGCGCTGACACCTAAATGAATGT 64771  
 Qy 611 -----LeuProLeu-----HisSerValLys----- 617  
 Db 64770 GTGATTCGAAATGATGATATCTTCTCACT--ATAAATACATTTATTGAGACACTGATAAA 64713  
 Qy 618 -----SerIleLys-----SerAspPhe----- 623  
 Db 64712 ACTTGAAGAAAGTCTAAGCATTAAGATAGATTAAGTTCCTGATTTTGAATCAGGT 64653  
 Qy 624 -----IleAspLysAlaGluLeu-----SerThrGln-- 632  
 Db 64652 AATTTGATTAAGAGAGAAATGTTCTGTTTATGAACATCATCTTAAGTATGACAGGA 64593  
 Qy 633 -----SerLysGluIleSerL 638  
 Db 64592 TGATTAAGATACAGGTGACGCCCTTAATCCGAGTATTCAGGAGCAAGAGGT--TCTT 64535  
 Qy 638 eu-ProGluVal-----SerLeuLeuLysIleLeuLysLeuA 650  
 Db 64534 TATCTTCAGATTAACAAGCGTATGGCTGGGAGGTTATTTTGTCTGACTACTTTGTTT 64475  
 Qy 642 ----- 641  
 Db 64474 CCTCATCTATTTGACGGGACTAGTATGATATCCATCTCTTTCATGATTTATGAGATTA 64415  
 Qy 650 snLys----- 651  
 Db 64414 AATAGTTGGTAAAGTTAAAGAGTTATTTAGTCCCTAGTTAAAGTTGGCTAGTTTGGAG 64355  
 Qy 651 ----- 651  
 Db 64354 TACCTTATATATTAAGTCTCAACTATATATAGAGATTAATAGTATTTATTTTGGAC 64295  
 Qy 652 -----P 652  
 Db 64294 CTTTCTCTATTTTGGCCCACTTTTATGATGTCCTTCCCTTCTGCGCTACTGTTTCTGTG 64235

Qy 652 roGluTrpProPheValValLeuGlyThrLeuAlaSer----- 664  
 Db 64234 CATGTGGT--TTCTTTCATATGCAACTCTTGCCCTCTCCACACAAAGCTTCAAGCTCC 64177  
 Qy 664 ----- 664  
 Db 64176 AAAAGACGTGAGTACAGACAGATGGGTATTCCTTGATGATTAATATATCTTACCAA 64117  
 Qy 665 -----Valle 666  
 Db 64116 TGAAGAGATTAATTTGTGTGAACGGTAAATGTACAAAAATATACAAAAATCTCATTTT 64057  
 Qy 666 uAsnGlyThrValHisProValPheSerIle----- 676  
 Db 64056 TACAGTTCTATATATGCAAAATTTTTCATTCGAAATAGAGATTAAAGATTCCTTACAA 63997  
 Qy 677 -IlePhe-----AlaLysIle----- 681  
 Db 63996 CATTTTGAAGGTATTAATTTGATTTATGATTAATTAATTAATTAATTAATTAATTAATTC 63937  
 Qy 681 ----- 681  
 Db 63936 TCTTCTTTTACTCTCCGTGAATATGAAATATGTAACCTTCTAAAGAAATTAATATGC 63877  
 Qy 682 IleThr-----MetPheGlyAsnAspLys-----ThrThrLeuLysHis-- 695  
 Db 63876 ATTAACCTCAAGCCATCTTTTSCAAAACCT--AAATTTAAGTACATGCTCATATATGATGT 63818  
 Qy 696 -----AerAlaGluIleTyr----- 700  
 Db 63817 ATGTAATACTGTATCTTATGCTAGTATTAATTAATTAATTAATTAATTAATTAATTC 63758  
 Qy 700 ----- 700  
 Db 63757 TACGAATGTGATTAACAATTATTAATTAAGAAATATGTAATAAATGCTTAATAAGATA 63698  
 Qy 701 -----SerMetIlePhe-----ValIleLeuGly----- 708  
 Db 63697 GACTCTTCTTTAGTTTGTGTTTGTTAATATGATATATATCTGTGATTTTCAACATCAGC 63638  
 Qy 709 -----ValIleCys-----PheValSer 714  
 Db 63637 TTATTAACAAGAACTTATCTGTAAGTGAAGGTGAAGATGACAGGGGTATGATCT 63578  
 Qy 715 TyrPheMet-----GlnGlyLeuPheTyr--GlyArgAlaGly----- 726  
 Db 63577 ATGTTTATGACAAATGAGATGTTGTATTAATGCTGGGTGTTGGGTGAAGAAACAAG 63518  
 Qy 727 -----GluIleLeuThrMetArgLeu- 733  
 Db 63517 AAGATATGGGTATGTAATCATATGATTAAGAGACAAAGAAATCTGTAACTTCACTTT 63458  
 Qy 734 ArgHis-----LeuAla----- 737  
 Db 63457 CAACACATCAATCTGACATGGGCTGTAAATCTGCTAAACTATTAAGAGAGGCTTC 63398  
 Qy 738 -----PheLys----- 739  
 Db 63397 AGAGCCACATAAAGTCTCCCTTTAAGAGGTATTAATTAATTAATTAATTAATTAATTAATTC 63338  
 Qy 740 AlMetLeuTyrGlnAspIleAlaTyrPheAspGluLys--GluAsnSerThrGlyGly 758  
 Db 63337 ATCAATCTCTATATACAGTCTCTATATGATTAATCACTAAACTAAATCAAGTTCAATTTGA 63278  
 Qy 759 LeuThrThrIleLeuAlaIle--AspIle----- 767  
 Db 63277 C--ATCTCAATATTTGACATCAAGACATAAATAAATAGTATATATTTCTTACTAGTTAG 63220  
 Qy 767 ----- 767  
 Db 63219 GCATTTTGAAGGAGAGATCACTGAGGTACAGAGTTTGAGACAGCTTGCCAAATG 63160





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Db      60999 ATAGGATGCCAAGACATACCTGATCTGTTGCGTGAGCCTTAGACCTTCC 60940
Qy      839 ----- 839
Db      60939 ACCTTTTTCACAGATAGAGACCCTTGAGTTGTTGCTGTGTATAGTCTGAC 60880
Qy      839 ----- 839
Db      60879 TACCTAGCAATATGCGCTCAGAGACGTAAACAGTTGTTAGACCTCCTGTCTAAT 60820
Qy      839 ----- 839
Db      60819 TAAACATGCAATATTATATACATTTCTAATTATGAGCGCTAATTATGTTCTCA 60760
Qy      839 ----- 839
Db      60759 TCTTATTTTATGTCATGAGCCTTGTGCTATATGCGCTTGTACTTTCCTTAATGT 60700
Qy      839 ----- 839
Db      60699 ATCTTAGAGCACTGAGACTATACAAACAACCTCTAATCAATAGTCAATTGAGG 60640
Qy      839 ----- 839
Db      60639 CATTTCCCTATGCTTTTAATTAAGTCAATTACTAAATCAATTTAGAACTATAGACTAA 60580
Qy      839 ----- 839
Db      60579 TAAATATATCGCTCTTCTTCACTGTCAGTGTAGATTGGAAAAATTAACAACGTTT 60520
Qy      839 ----- 839
Db      60519 AGTTTAAAGACTTGAATGGGCGAGGCGCTGCTTACGCCGTATCCCAACTTT 60460
Qy      839 ----- 839
Db      60459 GGGAGCCGAGGAGGTGATCACAGGTCCAGAGTTGAGACCAGCCTGACCAACATGG 60400
Qy      839 ----- 839
Db      60399 TGAACCCCTGTCTCTACTAAAAATACAAAAATTAAACAAGTATGTGACACGCCCTGCA 60340
Qy      839 ----- 839
Db      60339 ATCCAGCTACTCAGAGGCTAAGGCAAGAAATCACTTGAAGCCAGAGGCAAGGTTG 60280
Qy      839 ----- 839
Db      60279 CAGTGAGCAAGATCGACACATGCACTCCAGCCTGGGCAACAGACAGACTCATCTC 60220
Qy      839 ----- 839
Db      60219 AAAAGAAAAAAGAAAGACTTGAATAGCTTAATAGTTTCTTAATGACTATTTCTA 60160
Qy      839 ----- 839
Db      60159 AGGCTGTGTAATATATTCATCCCTTCCATGTGAAAAATGGAATTTTTTAATGT 60100
Qy      839 ----- 839
Db      60099 TCATTCCTTTTATCTCATCTCTTGTGTTTCTCAAAATTTTTTATATTCATTC 60040
Qy      839 ----- 839
Db      60039 CTTTGTGTTTCTCAAAAGGTTTCAGCATCTCTATCCATTTCTTCAATATATATG 59980
Qy      839 ----- 839
Db      59979 AATCTTACAAATGAGGTTCTTAAATGCTATTTTAAATTAATGAGAAATTTAAACAC 59920
Qy      839 ----- 839
Db      59919 CAACATCAAAATTTGGAGAGAAATCTGTGTCTCTACAGACGTCCAGAAATCTAGTTCC 59860

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Qy      839 ----- 839
Db      59859 CTCCTACAAACCAAGTATTTCTTACAGAAAGGCCAAGTGTACCTGTCTCTGTCC 59800
Qy      839 ----- 839
Db      59799 CACAGTCAATCTGCCAATCTGGAACAGAAATGTGAAAAAGAGAGTTCTCTTCAAGC 59740
Qy      839 ----- 839
Db      59739 CAACACATGTTCTCATGTCCGAAAAGCTATTTAAACAAACTCTCTTCATTTGAAT 59680
Qy      839 ----- 839
Db      59679 CCCATGTAATATGATCTCTTATTAATATATATATGTGGAAGATTCATCAT 59620
Qy      839 ----- 839
Db      59619 TTGAATTAATGTCTTTTATCATTCACAGAGCCCAATATGAGAAATGCTTATCTCAT 59560
Qy      839 ----- 839
Db      59559 AAGAAATTTAATCAACATGCCATGTACTTCTGTAAATGTTCTGAGTCTTTAAGT 59500
Qy      839 ----- 839
Db      59499 TGCATTTTAAATCTTGTGTAGAAATAAATATATATGATTAATCTTATCTGTCTATC 59440
Qy      839 ----- 839
Db      59439 TTTTATTTTATTTTATTTTATTTTGAAGAGAGTCTCATCTGTGCCCAAGTGA 59380
Qy      839 ----- 839
Db      59379 GTGCAGTGATGATCTCAGCTCATGCAACTCCACCTCCAGGTTCAAGTATCTCGT 59320
Qy      839 ----- 839
Db      59319 GCCTTAGCTTCTGAGTAGCTGGGATTACAGACATGTGCCACATACCTGTATATTTT 59260
Qy      839 ----- 839
Db      59259 GTAATTTAGTAGACAGAGGTTTACATGTGGCAGGCTGTTTCAACTCTGACC 59200
Qy      839 ----- 839
Db      59199 TCAAGTAATCGCCGCCCTTGCCCTCCAAAGTACTGGGATTACAAATCATAGCCATGT 59140
Qy      839 ----- 839
Db      59139 GCCTAGCATCTGCTATCTTTTACTTGAATGTTCATAATTTGTAGAACTCTTTGCA 59080
Qy      839 ----- 839
Db      59079 TGTGAACATATAGCTTACTAATGTTTATCTCTGTATAGAACAAAGTTAATTGAA 59020
Qy      839 ----- 839
Db      59019 ATTCAGTATTAATGTAATGGGTTAACTTAGATCAGTAGACTAAATCTCAATTAAGACA 58960
Qy      839 ----- 839
Db      58959 TTTTCTTAAGCTTATCATCCAAAAGTGCATTTTCTATCTTATTTTCTGGAGGAAG 58900
Qy      839 ----- 839
Db      58899 GAAAGTAAGATATTTGTGAGAAACTTACTGATGATATACTTAATATGTCCAGT 58840
Qy      839 ----- 839
Db      58839 GTGAGTACTAGAAATTCACAAATGGAAAAAGATTAAACATTAATTTTATTTCTATAT 58780

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QY 840 -----Lysilealathrglualeugluvenileargthrlleval 853
Db 58779 TGNATGTCTCTGTTTATATAGATGCACTGAAGCTTTGGAGAAATATACCTATATAGTG 58720
QY 854 SerLeuThrArgGluIuIysalaPheGluMetTyrGluGluMetLeuGlnThrGlnHis 873
Db 58719 TCATTAAACAAGGGAAGAAAGCCCTTGAGCAAAATGATAGAGAGATGCTTCACTCAACAC 58660
QY 873 ----- 873
Db 58659 AGGTGATTATAGATTGATCTGACTTCAAAACTTAATTTTGTCTGTAAAGGCACTACT 58600
QY 873 ----- 873
Db 58599 CTCGAATGACTCGAGTGGTTTGCCTGCTAATTCATTGCTCTTGAGCCTTTCTTAATAT 58540
QY 873 ----- 873
Db 58539 GTCATGTCAATATTTCTCATATGACTTCAACAGAGAACTAGAGAGAAATTGAGGGCA 58480
QY 873 ----- 873
Db 58479 ACCCAATTAGAAATAATATTAGGTCTCTGACATTACATTAACTGTCTGTACTAA 58420
QY 873 ----- 873
Db 58419 GATATGACATTTTCTTATTTTCTGAGAAATATTATGAAATATACATACGAGAAAG 58360
QY 873 ----- 873
Db 58359 AAAATAAATATGCGGCGAGGGCGCTGTGTCTCACCTGTAAATCCAGACATTTGGAGG 58300
QY 873 ----- 873
Db 58299 CTGAGGTGGCGGATCACTTAAGTCAAGATTAGAGACCGCTGAGCAACATGATGA 58240
QY 873 ----- 873
Db 58239 ACCCATCTCTACTAAATAATGCAAAATTAAGTGGGTGTGTGTGTCACATTTGTATCC 58180
QY 873 ----- 873
Db 58179 CAGCTACTTGAGGCTGAGGCGAGAGATCACTGAACCTGGAGGAGAGGTTGAGTG 58120
QY 873 ----- 873
Db 58119 AGCTGAGATCATGCACTTACATCTCAATCTCAGCTAGCGGACAGCAAGAGAAAGAG 58060
QY 873 ----- 873
Db 58059 CTCGGCCCTTACATTAAATCCCTAAATAGTTTACATTTTAAATACGAATATATACATA 58000
QY 873 ----- 873
Db 57999 ATTAATGCACTTACACTTTTAATTTAACTAGTCCCTCTATACATTGACTTAGTAT 57940
QY 873 ----- 873
Db 57939 GCTTTTATATTACTTAAACAGAAAGTAGCTTTTACTCTTTTGACATCACTAGTAG 57880
QY 873 ----- 873
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Dd	48159	ACCAAGTCTCTAATCATATATCCAAATTATCTTCCAGCTCACTGTGATTTCTTGATC	48100
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Dd	48099	AGACTGAGCTTAAGTCTGACAGTGTGATTTTCTTGATTAATAAACAATTATAAAAA	48040
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Dd	48039	AAAAACCTTGTGATTTGGTAACTCAAACTCAGTGACATTTCTGTATATAGCTGGGT	47980
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Dd	47979	ATCAATATATTCAAATGCGACTTTTGAGCTTTAAACATTTCTGTAAATATCAGTCTAAA	47920
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Dd	47919	AAATGCTTGACATCACTGAATAAATAACAATTATATTAGTATTATTTTGTTTTATA	47860
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Db	30279	AGTGGTTCTGCACATGGAAGATTAAGAAACAAGAACTCATCAAGACTCTCTGAGAA	30220
Qy	1208	nArgAspIleTy:PhelysleuValaasnIagInSerValGln	1222
Db	30219	TCGAGACATATATTTTAAGTTAAGTGAATGCACAGTCAGTCAG	30177

Search completed: December 17, 2003, 15:16:53  
Job time : 327 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 17, 2003, 14:29:55 ; Search time 85 Seconds

(without alignments)  
2.289 Million cell updates/sec

Title: us-09-873-409-5

Perfect score: 6159  
Sequence: 1 MIIIGILIASVNGACPLMPL.....QELLRRDIYFKLVNAQSVQ 1222

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.1  
Ygapop 10.0 , Ygapext 0.1  
Fgapop 6.0 , Fgapext 0.1  
Delop 6.0 , Delext 0.1

Searched: 1 segs, 79611 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seg length: 0  
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1 summaries

Command line parameters:

-MODE=frame+;p2n.model -DEV=soft -Q=us-09-873-409-5 -DB=2341014\_1997  
-SUFFIX=pro -OUT=all1997 -MINMATCH=0.1 -LOOPEXT=0 -UNITS=bits  
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-THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=1 -MODE=LOCAL -OUTPMT=pro  
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO XLPXY  
-NEG SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6  
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : 2341014\_1997.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2587.29	42.0	79611	1	AC002486 AC002486

#### ALIGNMENTS

RESULT 1  
AC002486  
LOCUS AC002486 79611 bp DNA linear PRI 22-AUG-1997  
DEFINITION Human BAC clone RG367017 from 7p15-p21, complete sequence.  
AC002486  
AC002486  
VERSION AC002486.1 GI:2341014  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukavica; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE  
1 (bases 1 to 79611)  
AUTHORS Kallunki,J., Smith,A. and Gibson,A.  
TITLE The sequence of H. sapiens BAC clone RG367017  
JOURNAL Unpublished (1997)  
REFERENCE 2 (bases 1 to 79611)

#### AUTHORS TITLE JOURNAL

#### COMMENT

Waterston,R.  
Direct Submission  
Submitted (22-AUG-1997) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
SUBMITTED BY:  
Genome Sequencing Center  
Department of Genetics  
Washington University  
St. Louis MO 63108, USA  
http://genome.wustl.edu/gsc  
mailto:sapiens@watson.wustl.edu

NOTICE: This sequence may not represent the entire insert of this  
clone. It may be shorter because we only sequence overlapping  
clone sections once, or longer because we provide a small overlap  
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
all regions were double stranded or sequenced with an alternate  
chemistry; an attempt was made to resolve all sequencing problems,  
such as compressions and repeats; all regions were covered by  
sequence from more than one subclone; and the assembly was  
confirmed by restriction digest.

#### MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and  
sequencing collaboration between the NHGRI Chromosome 7 Mapping  
Project (Eric D. Green, Director), John D. McPherson in the  
Department of Genetics (Washington University), and the Washington  
University Genome Sequencing Center. For additional information  
about the map position of this sequence, see  
http://www.nhgri.nih.gov/DIR/GRB/CHR7 or send  
mailto:egreen@nhgri.nih.gov

#### SOURCE INFORMATION:

This clone is from a release of the human BAC library. The library  
contains cloned DNA from human sperm. See: Shizuya et al., Proc.  
Natl. Acad. Sci. USA 89:8794-7 (1992); Kim et al., Genomics  
34:213-8 (1996). The clone is available from Research Genetics,  
Inc. (http://www.resgen.com).  
VECTOR: pBlOBAc11  
Selection: chloramphenicol

#### NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RG086D03. The actual start of  
this clone is at base position 1 of RG367017. This clone is part of  
an unanchored island, orientation is unknown.

This clone contains STS SMS1805 (NID:g1113222).

#### FEATURES

source	Location/Qualifiers
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repeat_region	/tpc_family="L1" 1781..2410
misc_feature	/tpc_family="L1" 3374..3875 /note="probable ras-related (RAL) pseudogene; similar to (PID:g1346952)"
misc_feature	3429..3529 /note="similar to EST T29472 (NID:g611570)"
misc_feature	3550..3804 /note="similar to EST AA523370 (NID:g2264082) nt57d09.g1"
misc_feature	3810..4260 /note="similar to EST AA403045 (NID:g2055607) zv63c09.r1"
misc_feature	3903..44207 /note="similar to EST Z44835 (NID:g574005)"

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## Alignment Scores:

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Pred. No.:  2587.29
Percent Similarity: 13.63%
Best Local Similarity: 11.51%
Query Match: 42.01%
DB:          1
Length:      79611
Matches:     837
Conservative: 154
Mismatches:  209
Indels:      6081
Gaps:        28

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us-09-873-409-5 (1-1222) x AC002486 (1-79611)

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DB      56460 ATATATTTGGATGCTTTTCACGCTTTCTATATTGTACAAAGCTGCAGACCAAGTTA 56519
QY      14 -----Cys-----LeuPro-----LeuMetProLeuValleuGly-- 23
DB      56520 TATAGATGAATCTTTGATATATATTAATTAAGGTGAATTCCTTAAGTTGATTTGGGCT 56579
QY      23 -----
DB      56580 GACTATGATATAGTTTAAAGCTTTTATCAAAAGCTTTTGACGCTATCATATATTTTTTT 56639
QY      23 -----
DB      56640 ACCCTTCAGTTCCACCTACATTAACCTGATGACTCAATGAAAGCTTTTCATATGAAG 56699
QY      24 -----Glu-----MetSerAs 27
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QY      27 PAsn-----Glu-----LeuIleSerGly----- 32

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Db	58860	GAACAGTAGAGGTAGAGTATTCAGTAGAAGGTGAGATTCACAAAGATGCGATAC	589194
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[illegible]

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Dd	60479	ATAAACGATCAGTTGAGATTAAAGAACTTTGTCTTGAGAACCAATATGATCTGCTC	60538
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Dd	61019	TTTCTGTCAACATCCAGCATGTATACCAACAAGACTATGAGATATCAAAAAGTTGT	61078
QY	292	-----	292
Dd	61079	TCTTATTAGAAAAGGCCAAGATACTTGATTAATCTGTGTCTTATGTCTTCGCGC	61138
QY	292	-----	292

[illegible]

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QY 367 ----- 367
Db 63359 ACTAAGAACTTCCAGCTGTTTCTTAGAATATGCTTGAATATGTTAGTAGT 63418
QY 367 ----- 367
Db 63419 CCTAAGAGAGCTTCATTAATAGCTTGGAATAATCTGGCAAGATCTCATTTACTTG 63478
QY 367 ----- 367
Db 63479 TTACAAATTAAGACTTCATTACCTGTAGTCAAAATTCATATATAATATTTAGTTGA 63538
QY 367 ----- 367
Db 63539 AATATGAAAGCTTACTAGTTAATTTCTGAAGTACTTAAATTTAGTTCTCTTACAT 63598
QY 367 ----- 367
Db 63599 AGAGAGATTAATGATAGATCTTTTACTACTATTTTCTGAATTTTTCAGGCTATTACTAC 63658
QY 367 ----- 367
Db 63659 ACATGTACATGAACAAACATTAACAAGATCTAAATTTGTTTGAAGAATTTGTTTGG 63718
QY 367 ----- 367
Db 63719 GTTAAATTAATGATCTCATTTTCTGAANAATGTCATCATCTTATTTGTGTTTAT 63778
QY 368 ----- 379
Db 63779 GATTTCCTCCATACATTCATCAATAGATTTCTGAAGAAGCTGAAATCTCAAGATTAAGCTG 63838
QY 379 |yglu|hr|val|ala|leu|val|gl|yleu|ang|lyse|gl|yl|y|se|th|val|val|gl|leu| 399
Db 63839 GAGAGACAGTCCCTGCTGCTCTCAATGCGAGTGGAGAGACGAGTGTCCAGCTTC 63898
QY 399 |eu|gl|na|rg|leu|ly|asp|pro|asp|asp|ly|phe|----- 409
Db 63899 TCGAGAGGTTATATGATCCGATGATGCTTTGTAGTGCAGTACGAAAAACATGACA 63958
QY 409 ----- 409
Db 63959 GTCCACCTAATGAACTCGAAGAACACCGCAGGCTGCAGCTCTGTAACTTTTCATTTTC 64018
QY 409 ----- 409
Db 64019 AACAGTAGAGCTGGAGAGAACCATATTTGTTTCTTCTTGTATCATTCACCTCAGC 64078
QY 409 ----- 409
Db 64079 AAATTAATTTATTAAGAGCTACTATGTGTACGACCTGTTTAAAGTCTGAGAAATACCTAG 64138
QY 409 ----- 409
Db 64139 GTGAATTAATAACAGATATAAAATCTGCCCTCATGAAGTTTACATTTTAATATCAGAGCAG 64198
QY 409 ----- 409
Db 64199 ACAATAAAAAAATAGATTAATTAATATAGTATGTAGAGAGGAGGAATGTTGTGAGAAA 64258
QY 409 ----- 409
Db 64259 AATAGCGTATTAACATCTGTACCCAGTACCTATCAAGAAATTTCAAAAGTTTGTCCAGAG 64318
QY 409 ----- 409
Db 64319 AATGATGTAGAAAAACATCTCCACTTTTCTTTTCTTTTCTTTTCTTTGAGCTTACAG 64378
QY 409 ----- 409
Db 64379 TGTTCACCTTAACCTTCTCAGCCTTGTAAAGTGATAGAGATTAAGACAGTGAATTTCA 64438
QY 409 ----- 409

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Db 64439 AAGTAAATTAATCTTAATGCTTCTCTTCAAAAGTTTCAACAGTATTTTAAAAAGAAATC 64498
QY 409 ----- 409
Db 64499 TACTCCCTAGAGCCTGGCTTATTTAATTTTACTTCATAGTTTTCATTTGGAGTATCC 64558
QY 409 ----- 409
Db 64559 TAGACCATGTGACTAATAATTAATAGATGATGTATGTATGTATTAAGAGTTGCATA 64618
QY 409 ----- 409
Db 64619 GAATATTCATGCCCTGACAGAAAAACAAGGTTGTAAGAAATAGAGACTTATGAGTTAG 64678
QY 409 ----- 409
Db 64679 AATTACAAACCTCGCTTCTGTACGGGAATATGTTGGGTAAATGGCAATGGCACAC 64738
QY 409 ----- 409
Db 64739 CCGTGAGAGACGAGTCACTTATATCATGTAGACAAATGAAGAGACACTTTTG 64798
QY 409 ----- 409
Db 64799 TCTTTTGACAGGTGTGAGATGTTGAATATAGCCGCTATTTCTTAAGAAATGTAG 64858
QY 409 ----- 409
Db 64859 GGTCAATCCAAACTGAAGTTTTTTGTATGTGTCTACATATTAACATTTGGGAACTTA 64918
QY 409 ----- 409
Db 64919 GAGTATGATCTTATTAATATCTAATCTGTGATCTTGAATAAGATATACATGATC 64978
QY 409 ----- 409
Db 64979 TGGCAAGTTTGAAGCAATTAATTTCTTTCAGTTTGTGTGCCATCTACAGAAA 65038
QY 409 ----- 409
Db 65039 AGCTATGACATATATATATGTAGAAATATTTATCAAAATATAGCTTTGATTT 65098
QY 409 ----- 409
Db 65099 CTAAATATGCTACTTCTCAGCTTATATTTGCTATGATGAAAAACCTTAATCAAT 65158
QY 410 ----- 415
Db 65159 ACAGTAAAGGCATCAACACATGTTCAATCTTTGATGGACATCATGTGATGAGA 65218
QY 415 |sna|sp|le|ar|ga|ala|leu|asn|val|arg|ile|tyr|arg|asp|his|ile|gl|val|ser|glng 435
Db 65219 ATGACATCAGAGCTTTAAATGTCGGCATTTATGAGAACCATATTTGGAGTGTATGCAAG 65278
QY 435 |u|p|ro|val|leu|phe|gl|y|th|th|ile|ser|asn|asn|ile|y|s|tyr|gl|y|arg|asp|asp|val|t 455
Db 65279 AGCCTGTTTGTTCGGGACCAACCATCATGTAACATATCAAGTATGACGAGATGATGTGA 65338
QY 455 |hr|asp|gl|u|me|gl|u|arg|ala|arg|glu|ala|asn|la|tyr|asp|phe|le|me|glu|p 475
Db 65339 CTATGAGAGATGAGAGAGAGACGACAAAGGAGAACAAATGGATATGATTTATCATGAGT 65398
QY 475 |he|p|ro|asn|----- 477
Db 65399 TTCTAATGTGATACACTGTGACGCTGTGTCTTAGCTTATGTGTGACGCGCTGGAC 65458
QY 477 ----- 477
Db 65459 ATTCAATATTAAGTATGAACAAACAACATGATGAGAAATAGAGGGGTGTGATTAATT 65518
QY 477 ----- 477

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Db 65519 CTGATTTCTTGAACAAGCTTGTCCAACTAGTGCACAAAGATGCTTGAATGAGTTC 65578  
 QY 477 ----- 477  
 Db 65579 CAACACAATTGTTAACTTTCTTAAACATTAAGATTTTGTGATTTTAAATC 65638  
 QY 478 ----- LysPheA 480  
 Db 65639 TTATCAGCTATTGTATTTAGTATTTAATGTGTGCCCAGAACATTTCTTTCA 65698  
 QY 480 sm-----ThrLeuValGlyIleValGln---M 490  
 Db 65699 ATGTGGCCAGGAGACCAAAAATTTGGACATCTGTATGAAACATCTGAGAGAAGA 65758  
 QY 490 ee---SerGlyGlyIleValGlnIleValIleValGln----- 502  
 Db 65759 TGCATATGTAACAACAAAGAAAGAAATGCAATTAAGCCAGATTGAAAAGATCAT 65818  
 QY 503 -----AlaLeuValArgAspProLysI 510  
 Db 65819 ATTTTCTTCTGCAATTGAAAAAGAAAAATGAAAGATATGTTAAAGCATTAACAAAGAA 65878  
 QY 510 le-----LeuIleLeuAspGlnIleThrSerIle----- 519  
 Db 65879 TATGAACAATAATCATCA--GACCAAGCTGAGAAATTAATGCTAAATGTTATTGGCA 65936  
 QY 520 -----LeuAspSerIleLysSerIleValGln----- 529  
 Db 65937 GGCATCTTGTGCTGAGAGTGGGAAAGTCATACACAAATGTTCAAGATTGTTCTGTGA 65996  
 QY 529 ----- 529  
 Db 65997 CAACCAACAAGAAACTATGATCATTTTAAAGCAGAGAACTTAACATTGCATAGA 66056  
 QY 529 ----- 529  
 Db 66057 AATGTGAATCAAGCCGGGTGCGGTGCTCACGCTGTATCCAGCACTGTGGAGGCC 66116  
 QY 529 ----- 529  
 Db 66117 GAGGTGGCAGATCACCTGAGTTAGAGTTGAGACCAAGCTTCGCCAAGGTGAAAA 66176  
 QY 530 -AlaIleLeuGlyIleAlaSerIle-----Gly---ArgThrIleValI 544  
 Db 66177 TTCATCTCTAATAAAGACAAAATAATAGCTGGGTGTGTGGCCACCTAATAGTCT 66236  
 QY 544 aAlaIleIleArg----- 547  
 Db 66237 CAGCTACTAGGAGGCTGAGGAGAGAAATCACTTGAACCTGGAGGTGAGATTGCAAT 66296  
 QY 547 ----- 547  
 Db 66297 GAGCTGAGATCGACCACTGCTCCACTGAGCAACAGATGAGACTTTATGGAAAA 66356  
 QY 547 ----- 547  
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 QY 547 ----- 547  
 Db 66417 AAGCATATATAGTAAGTAAATATTATTAAACAGACTTACGAGATCTTAATGGTATTT 66476  
 QY 548 -----LeuSer---ThrIleArgSer- 553  
 Db 66477 AGAATTAATGGGGTGTCTTAAGCTTTTAAATAATATTCTTGAAGTATTAATCTT 66536  
 QY 554 -----AlaAspLeuIleValIleThr----- 559  
 Db 66537 CAGATCCCTCGTAATTTGTTGTGCGAGCACCTTGTTCATATAGAAAGATGAGATTTC 66596  
 QY 559 ----- 559  
 Db 66597 AATTAAATCATATATAATTCCACATCCAGAGGGTCAATTAACAGAAATGTTTAT 66656

QY 559 ----- 559  
 Db 66657 TTAATGGCATATTTCACAACCAAACTTGAGGACTGTAAATTAATTTATCTTGTTT 66716  
 QY 559 ----- 559  
 Db 66717 TAATTTAAAAATTTGTATAGCCAGTAATTTGTTCTTGTCCCATTAATTTAGATCATTA 66776  
 QY 559 ----- 559  
 Db 66777 TTAGGACATATTTAGGCCAAAAAATCATTAAGATTAAAGTCTTAAATCTTGG 66836  
 QY 560 -----LeuIlePhe 562  
 Db 66837 GAACACACATTTCTTTTGTGATGTTTGGCCCTTTCATAGACTTCTTTCTTAAAC 66896  
 QY 562 polyMetLeuAla-----GlyIleGlyIle-----HisAl 572  
 Db 66897 ATCAATGCTCTCATTTCCACATTAAGATTAGGAGCTTCTGATGCTCTTAATCATAC 66956  
 QY 572 a-----GluLeuMetAlaIleValGlyLeuIleIleValIle----- 583  
 Db 66957 CCTGTAGTTACTACTGCTTTCACCAAGCCAAATCTACACAAAGATGTCCTTGTCT 67016  
 QY 584 -----LeuValMetSerGlnAspIleIleValIle----- 593  
 Db 67017 ATTAATCTAATTAATTAATTCAGAGATTAACCAAAATTAATTAAGATAGTACTTAT 67076  
 QY 594 -AspGluIleMetGluSerMetThrIleSerThrGlu-----ArgIleThrAsnSer 610  
 Db 67077 ATGATGAAC-CTAATTCACAGCGCATAGCTTAACCAAAAAATGAGAAACATATAT 67135  
 QY 610 ----- 610  
 Db 67136 GAATGAAGTTCAGAAAGTGGCTAATTTAGTAGTAATAAAATTTGGGAAAGCTATTGTA 67195  
 QY 611 -----LeuProLeu----- 613  
 Db 67196 AAAAATGTATTAACATTACTTCCCTTAATATATATACACAGATTTTAAATTAATGATAT 67255  
 QY 614 -----ValIle----- 617  
 Db 67256 AATTAGCTATCTGTGTTAGCTTTCATCATTAACACCATGAATTTGATTAACATA 67315  
 QY 617 ----- 617  
 Db 67316 TGAGCCAAAGGCAATTTCCATGATGATGATGAGAGTAAAGATGATTCCTTA 67375  
 QY 617 ----- 617  
 Db 67376 ACAGAGAGAAATCTCAATAAGTACTCATGAATTTGTCTGGAACTAGCTGAAG 67435  
 QY 617 ----- 617  
 Db 67436 GCAAGCTCAATTTTCAGGCGAGCTTGGCAGCTGAGAAAGTGAATGAATCACTGTG 67495  
 QY 618 -----SerIleIlePhe----- 621  
 Db 67496 GCGATGAGCAGGGGAGAAAGCCAGTGTATAGGCAATCCCTCAGAAATCTTGTCTGA 67555  
 QY 622 -AspPheIleAspIleValGln---GluSer----- 630  
 Db 67556 GATTAAGTACTTACTTCCAGAGCTCACAGAGAGTGGACCATTAAGCTGCAAGCGGAA 67615  
 QY 630 ----- 630  
 Db 67616 CACTGTATGAAGTCAAGCAGTCTGCGGGGCGTTGAAGTGCAGCGCAGCTGATGG 67675  
 QY 630 ----- 630  
 Db 67676 AGAGATCAATTAACACTTTTAAACCCCGCAGGCAAGTAGCTAAACCAAAAAAGCC 67735

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QY 630 ----- 630
Db 67736 ACACTTAGAGTCAGGACCAACCTTAGATCTACCTGCTCAACAACTGA 67795
QY 630 ----- 630
Db 67796 GACCAAGCCATGACAGATGCCAGAGAGAGAGGTTTGGAGGTGTGTTGCCAAGT 67855
QY 631 ----- 631
Db 67856 TATGTCCTTCTACAAATTCACCCCAAGAACTTAATGAAGATTGCAAGTTCAA 67915
QY 634 ysgLulleseer-----LeuPro----- 639
Db 67916 GATCAGTCAGTGTCTTGAGTTGCCCTACAGACAAATAATCAGCAGCTGTTTTTTTGT 67975
QY 640 ----- 640
Db 67976 TTTGTTTTTTTTCAGAGAGAAAAGAACTTAGAGTCTTCAACAACAATATACAGT 68035
QY 646 eLeuLyS-----LeuAsnLySProGlu----- 655
Db 68036 ACTCAGTACATCATTTACAAAAACCAAGACATGCAAAAGAAAGAAATATGCTGTAT 68095
QY 656 ----- 656
Db 68096 GCAAGAAACATATCTTAAAGTTTATCTTAGAAAGGCTTCAAAATATACGAAGC 68155
QY 658 ----- 658
Db 68156 AAAAATGATATACATGAAAGAGAAAGAAATCAAACTTAGTTAGGCGCTTCACT 68215
QY 658 lleu-----GlyThreLeuAla-----SerValLeuAsnGly 668
Db 68216 GCTTGATAGAAACAGCAGGTGATATCAGTAAGAAATATAGTAACAATATCTACAGGC 68275
QY 669 ----- 669
Db 68276 AGCTAGATTTCACTGCACTTATATACGATCTCCAGCAACAACAGAGAAATACATCTCA 68335
QY 676 ----- 676
Db 68336 AGTGCACACGCAACATCTCTAAATAA--ACAATATCTGGGCCATCAAAACAAACAA 68393
QY 686 ----- 686
Db 68394 ACAAACTGATAGCTCTTCAATTAATAGAAACATAGAAATATGTTCTCAGACCATAT 68453
QY 689 ----- 689
Db 68454 ATAACTAACTACACAATATTTGAAAAATCAAAAATCTAAAGATATATATATC 68513
QY 696 --AspAlaGluLe-----TyrSer----- 701
Db 68514 TCAAAAAAGAAATTTCAAGAAATGAAAACTATTTCTGAATCAAAATGAAATTTG 68573
QY 702 ----- 702
Db 68574 CAATGATATGATATTTTGTGAGATATAGTTAAAGTATGCTGTGAGAGAACTTATAGTAT 68633
QY 712 heValIserTyrPhe-----MetGlnGly-----LeuPhe--Tyr 722
Db 68634 TTATATGCTTATTTTCGAGAAAAAGAAAGATCTACAGTGTGCAAACTTAATTTTCACCTA 68693
QY 722 r-----GlyAlaGlnAla----- 725
Db 68694 CAGAACTAGAGAGAGAGAAATTAACCCAAAGACAGACAGATAGTAATATAGAAA 68753
QY 725 ----- 725
Db 68754 TTACAGTAGAAATCATGTAACCAAAACCTGAAGAAATCAATTAAGTAACCAAAAGCT 68813
QY 725 ----- 725

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Db 68814 GATTCACTGAAAAAGATTTAAAAAAGTAACTAGCAAGCTGAAAAAGAGA 68873
QY 725 ----- 725
Db 68874 GAGAGAGAGAAAAAGATGCGCAGTATCAGAAATGAAGAGGTACATGATTTGATTC 68933
QY 726 ----- 726
Db 68934 TAAGACATTAAGGTTAATAAAGTAATTAAGACGTGGGCAATTTTGAATTAAGT 68993
QY 731 ----- 731
Db 68994 CCTGTAATCCAGCACTTTGGAGGCTGAGGCTGATGATCACTTGAAGAGAGTTTG 69053
QY 737 ----- 737
Db 69054 TTACAGGCTGGCAACATGGCAAAACCTGTCTCTACTTAATAATCAAAAATTAAGCTG 69113
QY 748 p-----PheAspGlu-----LysGluAsn----- 754
Db 69114 GGTGTGTGTGTGACACCTGTATCCAGCTACTCGAAAGGCTGAGACAGAGAAATCAGT 69173
QY 755 --SerThrGlyLeuThrThrIleLeuAlaIleAspIleAlaGlnIleGlnGlyAlaT 774
Db 69174 TGAATCAGGAGGCA--AAGTTGACATGAGCT--GAGATAGCACACCTGACTCCAGCC 69229
QY 774 hrGlySerArgIle----- 778
Db 69230 TGGGCAACAGAGACAGACTGTCTGCTCCCGCAGCTCCCGCCAGCCCAAAAAAGCTA 69289
QY 779 ----- 779
Db 69290 GATGTCTAATATACGGCAACAGTATACAAATGAATTAATAAAGCAGTATTCACAA 69349
QY 783 ----- 783
Db 69350 GCATCAACAGACAAAATGCTTAAGAAATTAAGAAAGACGTGCAAGTCTTATAGTA 69409
QY 788 ----- 788
Db 69410 AAAATATATATATGCTGATAGACATGAAAAAGATCTAAAGAAATGAAGATCTTATCA 69469
QY 788 ----- 788
Db 69470 TTGATTTAGAACTCATATTTTAAAGATTGCAATCTCTCCAGTTGATATATAATA 69529
QY 789 ---GlyLeuSerValIleIleSer-----PheIleTyr----- 798
Db 69530 TTGTGCTTATCAATCAAAATCTCACAGTTTATATGATGTGTAGAAACTGACATGT 69589
QY 798 ----- 798
Db 69590 TGAATCCAAATTTATTTGAAATTCAAAAGACCAACATAGCCAAACAAATTTGAAG 69649
QY 798 ----- 798
Db 69650 AAAGACCAAGCTGAGAGACCTTAATATCTAATTTTAAGACAGCATTAAGATCGGTGA 69709
QY 798 ----- 798
Db 69710 GTGCAATATGATGTTGTATAGATCAGTACATGGAACAGAGACAGAAATAGATTTC 69769
QY 798 ----- 798
Db 69770 ACAATATCTACTAAGTTAATTTTGAAGAGCGGAATGAATCACTAGTGGGGAAGAAAT 69829
QY 799 ----- 799
Db 69830 ATCTTTCAACAATAGTGTGTGAGAACAAATGTTATCTTTGAGAAAAATTAATAAGTGA 69889
QY 803 hrPhe-----LeuIle--LeuSerIleAlaProValLeu-- 813

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QY 1064 Glu-----ProValleuPheAsn-----Cys 1070
Db 72077 CAATTTTCTGATGCTCTCTCTTTGGGCTCTTTTCTTTTACAGCGTTGT 72136
QY 1071 SerIleAgluAsnIleA-----1077
Db 72137 TTTCACAAGAACAAATCAAAAGACATTAAGCACCAGGCTGAAGTACTGATTAAGCTG 72196
QY 1078 -TyrGlyAspAsnSerArgValVal-----ProLeuAspGluIleLeuGlu 1092
Db 72197 ATATTAAACACAACTGGAGATTCCTGCTTCAACATTTGAT-----72244
QY 1093 AlaIleAsnIleAAsnIleHisSer-----PheIleGluGlyLeuProGlu---- 1108
Db 72245 -----CACGCTGCTTCTGTTCTGTTCTGTTCTTCTTCTATTTTTC 72283
QY 1109 -----LysTyrAsnThrGlnValGlyLeuGlyValGlnLeuSerGlyGlyGlnLysG 1127
Db 72284 ATTAGAAATTTAATACATGTGTAGGGGMAAGAGCTCAATGATGAGGGCAGAAAC 72343
QY 1127 IlnArgLeuAlaIleAlaArgAlaLeuLeuGlnLysProLysIleLeuLeuAspGluA 1147
Db 72344 AGAGGATCGCAATGCTGTGCTTGAAGTCCATGCGAAACCCAGATTCGTGATTTAGATGAG 72403
QY 1147 IlnThrSerAlaLeuAspAsnAspSerGlyLysValGlnHisAlaLeuAspLysAla- 1166
Db 72404 CTACGTCTGCCCTGGATTCAAGAAAGCAAGTCAAGCTGTTCAAGCTGCACTGGAGAAAGTAA 72463
QY 1166 -----1166
Db 72464 GTGAGCAGAAACGTTCTTATTTCCATCTCTGTTTCATTAATGTTTGAAGTACAAGA 72523
QY 1166 -----1166
Db 72524 AAGTAAAGATCTGTAATAGATTACTCAAGTTGAGAGCCCTCTTAAGTAAAGCAGGA 72583
QY 1167 -----ArgThrGlyArgT 1171
Db 72584 TGTTAATCCACTGAGAACTTAACGTGATGGCTATAGAAAGTGTATTAGAGGACAGA-AGGA 72642
QY 1171 hrCys-----LeuVal-----ValThrHisArgLeuSerAla 1181
Db 72643 GATGCTGTGTGGTGGTGTGTAATAAATATATATACATGAGGCTGATACACAAACATCATCC 72702
QY 1181 -----1181
Db 72703 AGTCTAATCTCCATTCACAGTGTGGCTTTCACCTCTCTAGAGTGCCCACT 72762
QY 1181 -----1181
Db 72763 ATCATCACTAATTATACCATGCCACCCCTTGTCTTCTTCAATACACCTGTGGATTCT 72822
QY 1181 -----1181
Db 72823 CTTCCTGACCACTTCTTCTTTAGAGTACCCCAAGTATTCATTTGACCTAATTTC 72882
QY 1182 -----IleGlnAsn-AlaAspLeu-----1187
Db 72883 CCTCAAGTGGAAATCGCTGACCTTGAACACAGCGCCCTTGACAGCTCTGCCCCCTCAA 72942
QY 1188 -----1188
Db 72943 CCTGACCTGACCTCTGCTGCTATGAGTACTGACATACCTCAAGCCCATATGCACT 73002
QY 1188 eValValleuHis-----AsnGlyLysIleLys 1197
Db 73003 TGTGGCCCTGACCAAAATTACCTGAATCTAGAGAGGAGTGGCAGTGGCGGTATGAAA 73062
QY 1198 -----GlnGln-----1199
Db 73063 AACCATTTGAACAGTTTCTCGATGCGCTGACTCCCTTATTAACAGAGCCTTCAGACCCC 73122
QY 1200 -----GlyThr-----His-----GlnGluLeu-----1205

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Db 73123 TTACAAGCTTAATGGACATTTTACTTTCATTTGCTTGAAGTGAAGTTAAGCGTTT 73182
QY 1206 -----LeuArg-AsnArgAspIle--TyrPheLysLeuVal-----AsnAlaGln 1219
Db 73183 TTTCCTTAAGAAATCGCAGGCTTCTTTTAAATGCTGACTTTATGAAACAGAAA 73242
QY 1220 SerVal 1221
Db 73243 CGGATA 73248

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Search completed: December 17, 2003, 14:33:16  
 Job time : 200 secs